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agagaaccta ttgaagtgaa cctgtttgga ctcatcagtg tgacactaaa 550

tatgcttcct ttggtcaaga aagctcaagg gagagttatt aatgtctcca 600

gtgttggagg tcgccttgca atcgttggag ggggctatac tccatccaaa 650

tatgcagtgg aaggtttcaa tgacagctta agacgggaca tgaaagcttt 700

tggtgtgcac gtctcatgca ttgaaccagg attgttcaaa acaaacttgg 750

cagatccagt aaaggtaatt gaaaaaaaac tcgccatttg ggagcagctg 800

tctccagaca tcaaacaaca atatggagaa ggttacattg aaaaaagtct 850

agacaaactg aaaggcaata aatcctatgt gaacatggac ctctctccgg 900

tggtagagtg catggaccac gctctaacaa gtctcttccc taagactcat 950

tatgccgctg gaaaagatgc caaaattttc tggatacctc tgtctcacat 1000

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ctaatcccaa ggcagtgtga ctcagctaac cacaaatgtc tcctccaggc 1100

tatgaaattg gccgatttca agaacacatc tcctttttcaa ccccattcct 1150

tatctgctcc aacctggact catttagatc gtgcttattt ggattgcaaa 1200

agggagtccc accatcgctg gtggtatccc agggtccctg ctcaagtttt 1250

ctttgaaaag gagggctgga atggtacatc acataggcaa gtcctgccct 1300

gtatttaggc tttgcctgct tggtgtgatg taagggaaat tgaaagactt 1350

gcccattcaa aatgatcttt accgtggcct gccccatgct tatggtcccc 1400

agcatttaca gtaacttgtg aatgttaagt atcatctctt atctaaatat 1450

taaaagataa gtcaacccaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1500

aaaaaaaa 1508

<210> 10
<211> 319
<212> PRT
<213> Homo sapiens

<220>
<221> sig_peptide
<222> 1-17
<223> Signal Peptide

<220>
<221> misc_feature

17

<222> 36-47, 108-113, 166-171,198-203, 207-212
<223> N-myristoylation Sites.

<220>
<221> misc_feature
<222> 39-42
<223> Glycosaminoglycan Attachment Site.

<220>
<221> TRANSMEM
<222> 136-152
<223> Transmembrane Domain

<220>
<221> misc_feature
<222> 161-163, 187-190 and 253-256
<223> N-glycosylation Sites.

<400> 10

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Met Leu Phe Trp Val Leu Gly Leu Leu Ile Leu Cys Gly Phe Leu
 1               5                  10                  15

Trp Thr Arg Lys Gly Lys Leu Lys Ile Glu Asp Ile Thr Asp Lys
                20                  25                  30

Tyr Ile Phe Ile Thr Gly Cys Asp Ser Gly Phe Gly Asn Leu Ala
                35                  40                  45

Ala Arg Thr Phe Asp Lys Lys Gly Phe His Val Ile Ala Ala Cys
                50                  55                  60

Leu Thr Glu Ser Gly Ser Thr Ala Leu Lys Ala Glu Thr Ser Glu
                65                  70                  75

Arg Leu Arg Thr Val Leu Leu Asp Val Thr Asp Pro Glu Asn Val
                80                  85                  90

Lys Arg Thr Ala Gln Trp Val Lys Asn Gln Val Gly Glu Lys Gly
                95                  100                 105

Leu Trp Gly Leu Ile Asn Asn Ala Gly Val Pro Gly Val Leu Ala
                110                 115                 120

Pro Thr Asp Trp Leu Thr Leu Glu Asp Tyr Arg Glu Pro Ile Glu
                125                 130                 135

Val Asn Leu Phe Gly Leu Ile Ser Val Thr Leu Asn Met Leu Pro
                140                 145                 150

Leu Val Lys Lys Ala Gln Gly Arg Val Ile Asn Val Ser Ser Val
                155                 160                 165

Gly Gly Arg Leu Ala Ile Val Gly Gly Gly Tyr Thr Pro Ser Lys
                170                 175                 180

Tyr Ala Val Glu Gly Phe Asn Asp Ser Leu Arg Arg Asp Met Lys
                185                 190                 195
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18

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Ala Phe Gly Val His Val Ser Cys Ile Glu Pro Gly Leu Phe Lys
            200             205             210

Thr Asn Leu Ala Asp Pro Val Lys Val Ile Glu Lys Lys Leu Ala
            215             220             225

Ile Trp Glu Gln Leu Ser Pro Asp Ile Lys Gln Gln Tyr Gly Glu
            230             235             240

Gly Tyr Ile Glu Lys Ser Leu Asp Lys Leu Lys Gly Asn Lys Ser
            245             250             255

Tyr Val Asn Met Asp Leu Ser Pro Val Val Glu Cys Met Asp His
            260             265             270

Ala Leu Thr Ser Leu Phe Pro Lys Thr His Tyr Ala Ala Gly Lys
            275             280             285

Asp Ala Lys Ile Phe Trp Ile Pro Leu Ser His Met Pro Ala Ala
            290             295             300

Leu Gln Asp Phe Leu Leu Leu Lys Gln Lys Ala Glu Leu Ala Asn
            305             310             315

Pro Lys Ala Val


<210> 11
<211> 2720
<212> DNA
<213> Homo sapines

<400> 11
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gccccttggg ccgtcgccac cactgtagtc atgtacccac cgccgccgcc   150

gccgcctcat cgggacttca tctcggtgac gctgagcttt ggcgagagct   200

atgacaacag caagagttgg cggcggcgct cgtgctggag gaaatggaag   250

caactgtcga gattgcagcg gaatatgatt ctcttcctcc ttgcctttct   300

gcttttctgt ggactcctct tctacatcaa cttggctgac cattggaaag   350

ctctggcttt caggctagag gaagagcaga agatgaggcc agaaattgct   400

gggttaaaac cagcaaatcc acccgtctta ccagctcctc agaaggcgga   450

caccgaccct gagaacttac ctgagatttc gtcacagaag acacaaagac   500

acatccagcg gggaccacct cacctgcaga ttagacccc aagccaagac   550

ctgaaggatg ggacccagga ggaggccaca aaaaggcaag aagcccctgt   600

ggatccccgc ccggaaggag atccgcagag acagtcatc agctggaggg   650
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gagcggtgat cgagcctgag cagggcaccg agctcccttc aagaagagca 700

gaagtgccca ccaagcctcc cctgccaccg gccaggacac agggcacacc 750

agtgcatctg aactatcgcc agaagggcgt gattgacgtc ttcctgcatg 800

catggaaagg ataccgcaag tttgcatggg gccatgacga gctgaagcct 850

gtgtccaggt ccttcagtga gtggtttggc ctcggtctca cactgatcga 900

cgcgctggac accatgtgga tcttgggtct gaggaaagaa tttgaggaag 950

ccaggaagtg ggtgtcgaag aagttacact ttgaaaagga cgtggacgtc 1000

aacctgtttg agagcacgat ccgcatcctg gggggctcc tgagtgccta 1050

ccacctgtct ggggacagcc tcttcctgag gaaagctgag gattttggaa 1100

atcggctaat gcctgccttc agaacaccat ccaagattcc ttactcggat 1150

gtgaacatcg gtactggagt tgcccacccg ccacggtgga cctccgacag 1200

cactgtggcc gaggtgacca gcattcagct ggagttccgg gagctctccc 1250

gtctcacagg ggataagaag tttcaggagg cagtggagaa ggtgacacag 1300

cacatccacg gcctgtctgg gaagaaggat gggctggtgc ccatgttcat 1350

caatacccac agtggcctct tcacccacct gggcgtattc acgctgggcg 1400

ccagggccga cagctactat gagtacctgc tgaagcagtg gatccagggc 1450

gggaagcagg agacacagct gctggaagac tacgtggaag ccatcgaggg 1500

tgtcagaacg cacctgctgc ggcactccga gcccagtaag ctcacctttg 1550

tgggggagct tgcccacggc cgcttcagtg ccaagatgga ccacctggtg 1600

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accggcagat ggagacgggg ctgagtcccg agatcgtgca cttcaacctt 1750

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caacctgctg cggccagaga ccgtggagag cctgttctac ctgtaccgcg 1850

tcacagggga ccgcaaatac caggactggg gctgggagat tctgcagagc 1900

ttcagccgat tcacacgggt ccctcgggt ggctattctt ccatcaacaa 1950

tgtccaggat cctcagaagc ccgagcctag ggacaagatg gagagcttct 2000

tcctggggga acgctcaag tatctgttct tgctcttctc cgatgaccca 2050

aacctgctca gcctggacgc ctacgtgttc aacaccgaag cccaccctct 2100
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20

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gcctatctgg acccctgcct agggtggatg gctgctggtg tggggacttc 2150

gggtgggcag aggcaccttg ctgggtctgt ggcattttcc aagggcccac 2200

gtagcaccgg caaccgccaa gtggcccagg ctctgaactg gctctgggct 2250

cctcctcgtc tctgctttaa tcaggacacc gtgaggacaa gtgaggccgt 2300

cagtcttggt gtgatgcggg gtgggctggg ccgctggagc ctccgcctgc 2350

ttcctccaga agacacgaat catgactcac gattgctgaa gcctgagcag 2400

gtctctgtgg gccgaccaga gggggggcttc gaggtggtcc ctggtactgg 2450

ggtgaccgag tggacagccc agggtgcagc tctgcccggg ctcgtgaagc 2500

ctcagatgtc cccaatccaa gggtctggag gggctgccgt gactccagag 2550

gcctgaggct ccagggctgg ctctggtgtt tacaagctgg actcagggat 2600

cctcctggcc gccccgcagg gggcttggag ggctggacgg caagtccgtc 2650

tagctcacgg gcccctccag tggaatgggt cttttcggtg gagataaaag 2700

ttgatttgct ctaaccgcaa 2720
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<210> 12
<211> 699
<212> PRT
<213> Homo sapiens

<220>
<221> TRANSMEM
<222> 21-40 and 84-105
<223> Transmembrane Domain (type II)

<400> 12

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Met Ala Ala Cys Glu Gly Arg Arg Ser Gly Ala Leu Gly Ser Ser
 1               5                  10                  15

Gln Ser Asp Phe Leu Thr Pro Pro Val Gly Gly Ala Pro Trp Ala
                20                  25                  30

Val Ala Thr Thr Val Val Met Tyr Pro Pro Pro Pro Pro Pro Pro
                35                  40                  45

His Arg Asp Phe Ile Ser Val Thr Leu Ser Phe Gly Glu Ser Tyr
                50                  55                  60

Asp Asn Ser Lys Ser Trp Arg Arg Arg Ser Cys Trp Arg Lys Trp
                65                  70                  75

Lys Gln Leu Ser Arg Leu Gln Arg Asn Met Ile Leu Phe Leu Leu
                80                  85                  90

Ala Phe Leu Leu Phe Cys Gly Leu Leu Phe Tyr Ile Asn Leu Ala
                95                 100                 105
```

21

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Asp His Trp Lys Ala Leu Ala Phe Arg Leu Glu Glu Glu Gln Lys
             110             115                 120

Met Arg Pro Glu Ile Ala Gly Leu Lys Pro Ala Asn Pro Pro Val
             125             130                 135

Leu Pro Ala Pro Gln Lys Ala Asp Thr Asp Pro Glu Asn Leu Pro
             140             145                 150

Glu Ile Ser Ser Gln Lys Thr Gln Arg His Ile Gln Arg Gly Pro
             155             160                 165

Pro His Leu Gln Ile Arg Pro Pro Ser Gln Asp Leu Lys Asp Gly
             170             175                 180

Thr Gln Glu Glu Ala Thr Lys Arg Gln Glu Ala Pro Val Asp Pro
             185             190                 195

Arg Pro Glu Gly Asp Pro Gln Arg Thr Val Ile Ser Trp Arg Gly
             200             205                 210

Ala Val Ile Glu Pro Glu Gln Gly Thr Glu Leu Pro Ser Arg Arg
             215             220                 225

Ala Glu Val Pro Thr Lys Pro Pro Leu Pro Pro Ala Arg Thr Gln
             230             235                 240

Gly Thr Pro Val His Leu Asn Tyr Arg Gln Lys Gly Val Ile Asp
             245             250                 255

Val Phe Leu His Ala Trp Lys Gly Tyr Arg Lys Phe Ala Trp Gly
             260             265                 270

His Asp Glu Leu Lys Pro Val Ser Arg Ser Phe Ser Glu Trp Phe
             275             280                 285

Gly Leu Gly Leu Thr Leu Ile Asp Ala Leu Asp Thr Met Trp Ile
             290             295                 300

Leu Gly Leu Arg Lys Glu Phe Glu Glu Ala Arg Lys Trp Val Ser
             305             310                 315

Lys Lys Leu His Phe Glu Lys Asp Val Asp Val Asn Leu Phe Glu
             320             325                 330

Ser Thr Ile Arg Ile Leu Gly Gly Leu Leu Ser Ala Tyr His Leu
             335             340                 345

Ser Gly Asp Ser Leu Phe Leu Arg Lys Ala Glu Asp Phe Gly Asn
             350             355                 360

Arg Leu Met Pro Ala Phe Arg Thr Pro Ser Lys Ile Pro Tyr Ser
             365             370                 375

Asp Val Asn Ile Gly Thr Gly Val Ala His Pro Pro Arg Trp Thr
             380             385                 390

Ser Asp Ser Thr Val Ala Glu Val Thr Ser Ile Gln Leu Glu Phe
```

22

Arg Glu Leu Ser Arg Leu Thr Gly Asp Lys Lys Phe Gln Glu Ala
                410   415   420

Val Glu Lys Val Thr Gln His Ile His Gly Leu Ser Gly Lys Lys
                425   430   435

Asp Gly Leu Val Pro Met Phe Ile Asn Thr His Ser Gly Leu Phe
                440   445   450

Thr His Leu Gly Val Phe Thr Leu Gly Ala Arg Ala Asp Ser Tyr
                455   460   465

Tyr Glu Tyr Leu Leu Lys Gln Trp Ile Gln Gly Gly Lys Gln Glu
                470   475   480

Thr Gln Leu Leu Glu Asp Tyr Val Glu Ala Ile Glu Gly Val Arg
                485   490   495

Thr His Leu Leu Arg His Ser Glu Pro Ser Lys Leu Thr Phe Val
                500   505   510

Gly Glu Leu Ala His Gly Arg Phe Ser Ala Lys Met Asp His Leu
                515   520   525

Val Cys Phe Leu Pro Gly Thr Leu Ala Leu Gly Val Tyr His Gly
                530   535   540

Leu Pro Ala Ser His Met Glu Leu Ala Gln Glu Leu Met Glu Thr
                545   550   555

Cys Tyr Gln Met Asn Arg Gln Met Glu Thr Gly Leu Ser Pro Glu
                560   565   570

Ile Val His Phe Asn Leu Tyr Pro Gln Pro Gly Arg Arg Asp Val
                575   580   585

Glu Val Lys Pro Ala Asp Arg His Asn Leu Leu Arg Pro Glu Thr
                590   595   600

Val Glu Ser Leu Phe Tyr Leu Tyr Arg Val Thr Gly Asp Arg Lys
                605   610   615

Tyr Gln Asp Trp Gly Trp Glu Ile Leu Gln Ser Phe Ser Arg Phe
                620   625   630

Thr Arg Val Pro Ser Gly Gly Tyr Ser Ser Ile Asn Asn Val Gln
                635   640   645

Asp Pro Gln Lys Pro Glu Pro Arg Asp Lys Met Glu Ser Phe Phe
                650   655   660

Leu Gly Glu Thr Leu Lys Tyr Leu Phe Leu Leu Phe Ser Asp Asp
                665   670   675

Pro Asn Leu Leu Ser Leu Asp Ala Tyr Val Phe Asn Thr Glu Ala
                680   685   690

23

His Pro Leu Pro Ile Trp Thr Pro Ala
                    695

<210> 13
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 13
 cgccagaagg gcgtgattga cgtc 24

<210> 14
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 14
 ccatccttct tcccagacag gccg 24

<210> 15
<211> 44
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-44
<223> Synthetic construct.

<400> 15
 gaagcctgtg tccaggtcct tcagtgagtg gtttggcctc ggtc 44

<210> 16
<211> 1524
<212> DNA
<213> Homo sapiens

<400> 16
 ggcgccgcgt aggcccggga ggccgggccg gccgggctgc gagcgcctgc 50

 cccatgcgcc gccgcctctc cgcacgatgt tcccctcgcg gaggaaagcg 100

 gcgcagctgc cctgggagga cggcaggtcc gggttgctct ccggcggcct 150

 ccctcggaag tgttccgtct tccacctgtt cgtggcctgc ctctcgctgg 200

 gcttcttctc cctactctgg ctgcagctca gctgctctgg ggacgtggcc 250

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cgggcagtca ggggacaagg gcaggagacc tcgggccctc cccgtgcctg 300

cccccagag ccgcccctg agcactggga agaagacgca tcctgggggc 350

cccaccgcct ggcagtgctg gtgcccttcc gcgaacgctt cgaggagctc 400

ctggtcttcg tgccccacat gcgccgcttc ctgagcagga agaagatccg 450

gcaccacatc tacgtgctca accaggtgga ccacttcagg ttcaaccggg 500

cagcgctcat caacgtgggc ttcctggaga gcagcaacag cacggactac 550

attgccatgc acgacgttga cctgctccct ctcaacgagg agctggacta 600

tggctttcct gaggctgggc ccttccacgt ggcctccccg gagctccacc 650

ctctctacca ctacaagacc tatgtcggcg gcatcctgct gctctccaag 700

cagcactacc ggctgtgcaa tgggatgtcc aaccgcttct ggggctgggg 750

ccgcgaggac gacgagttct accggcgcat taagggagct gggctccagc 800

ttttccgccc ctcgggaatc acaactgggt acaagacatt tcgccacctg 850

catgacccag cctggcggaa gagggaccag aagcgcatcg cagctcaaaa 900

acaggagcag ttcaaggtgg acagggaggg aggcctgaac actgtgaagt 950

accatgtggc ttcccgcact gccctgtctg tgggcggggc ccctgcact 1000

gtcctcaaca tcatgttgga ctgtgacaag accgccacac cctggtgcac 1050

attcagctga gctggatgga cagtgaggaa gcctgtacct acaggccata 1100

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cgctgcttgc catgcacagt gatcagagag aggctggggt gtgtcctgtc 1300

cgggaccccc cctgccttcc tgctcaccct actctgacct ccttcacgtg 1350

cccaggcctg tgggtagtgg ggagggctga acaggacaac ctctcatcac 1400

cctactctga cctccttcac gtgcccaggc ctgtgggtag tggggagggc 1450

tgaacaggac aacctctcat cacccccaaa aaaaaaaaa aaaaaaaaa 1500

aaaaaaaaa aaaaaaaaa aaaa 1524
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<210> 17
<211> 327
<212> PRT
<213> Homo sapiens

<220>

25

<221> sig_peptide
<222> 1-42
<223> Signal peptide.

<220>
<221> misc_feature
<222> 19-25,65-71,247-253,285-291,303-310
<223> N-myristoylation site.

<220>
<221> misc_feature
<222> 27-31
<223> cAMP- and cGMP-dependent protein kinase phosphorylation site.

<220>
<221> TRANSMEM
<222> 29-49
<223> Transmembrane domain (type II).

<220>
<221> misc_feature
<222> 154-158
<223> N-glycosylation site.

<220>
<221> misc_feature
<222> 226-233
<223> Tyrosine kinase phosphorylation site.

<400> 17
Met Phe Pro Ser Arg Arg Lys Ala Ala Gln Leu Pro Trp Glu Asp
 1   5   10   15

Gly Arg Ser Gly Leu Leu Ser Gly Gly Leu Pro Arg Lys Cys Ser
                20   25   30

Val Phe His Leu Phe Val Ala Cys Leu Ser Leu Gly Phe Phe Ser
                35   40   45

Leu Leu Trp Leu Gln Leu Ser Cys Ser Gly Asp Val Ala Arg Ala
                50   55   60

Val Arg Gly Gln Gly Gln Glu Thr Ser Gly Pro Pro Arg Ala Cys
                65   70   75

Pro Pro Glu Pro Pro Pro Glu His Trp Glu Glu Asp Ala Ser Trp
                80   85   90

Gly Pro His Arg Leu Ala Val Leu Val Pro Phe Arg Glu Arg Phe
                95   100   105

Glu Glu Leu Leu Val Phe Val Pro His Met Arg Arg Phe Leu Ser
                110   115   120

Arg Lys Lys Ile Arg His His Ile Tyr Val Leu Asn Gln Val Asp
                125   130   135

His Phe Arg Phe Asn Arg Ala Ala Leu Ile Asn Val Gly Phe Leu

26

Glu Ser Ser Asn Ser Thr Asp Tyr Ile Ala Met His Asp Val Asp
155   160   165

Leu Leu Pro Leu Asn Glu Glu Leu Asp Tyr Gly Phe Pro Glu Ala
170   175   180

Gly Pro Phe His Val Ala Ser Pro Glu Leu His Pro Leu Tyr His
185   190   195

Tyr Lys Thr Tyr Val Gly Gly Ile Leu Leu Leu Ser Lys Gln His
200   205   210

Tyr Arg Leu Cys Asn Gly Met Ser Asn Arg Phe Trp Gly Trp Gly
215   220   225

Arg Glu Asp Asp Glu Phe Tyr Arg Arg Ile Lys Gly Ala Gly Leu
230   235   240

Gln Leu Phe Arg Pro Ser Gly Ile Thr Thr Gly Tyr Lys Thr Phe
245   250   255

Arg His Leu His Asp Pro Ala Trp Arg Lys Arg Asp Gln Lys Arg
260   265   270

Ile Ala Ala Gln Lys Gln Glu Gln Phe Lys Val Asp Arg Glu Gly
275   280   285

Gly Leu Asn Thr Val Lys Tyr His Val Ala Ser Arg Thr Ala Leu
290   295   300

Ser Val Gly Gly Ala Pro Cys Thr Val Leu Asn Ile Met Leu Asp
305   310   315

Cys Asp Lys Thr Ala Thr Pro Trp Cys Thr Phe Ser
320   325

<210> 18
<211> 23
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-23
<223> Synthetic construct.

<400> 18
 gcgaacgctt cgaggagtcc tgg 23

<210> 19
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence

<222> 1-24
<223> Synthetic construct

<400> 19
 gcagtgcggg aagccacatg gtac 24

<210> 20
<211> 46
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-46
<223> Synthetic construct.

<400> 20
 cttcctgagc aggaagaaga tccggcacca catctacgtg ctcaac 46

<210> 21
<211> 494
<212> DNA
<213> Homo sapiens

<400> 21
 caatgtttgc ctatccacct cccccaagcc cctttaccta tgctgctgct 50

 aacgctgctg ctgctgctgc tgctgcttaa aggctcatgc ttggagtggg 100

 gactggtcgg tgcccagaaa gtctcttctg ccactgacgc ccccatcagg 150

 gattgggcct tctttccccc ttcctttctg tgtctcctgc ctcatcggcc 200

 tgccatgacc tgcagccaag cccagccccg tggggaaggg gagaaagtgg 250

 gggatggcta agaaagctgg gagatanggga acagaagagg gtagtgggtg 300

 ggctagggg gctgccttat ttaaagtggt tgtttatgat tcttatacta 350

 atttatacaa agatattaag gccctgttca ttaagaaatt gttcccttcc 400

 cctgtgttca atgtttgtaa agattgttct gtgtaaatat gtctttataa 450

 taaacagtta aaagctgaaa aaaaaaaaaa aaaaaaaaaa aaaa 494

<210> 22
<211> 73
<212> PRT
<213> Homo sapiens

<220>
<221> sig_peptide
<222> 1-15
<223> Signal peptide.

<220>
<221> misc_feature
<222> 3-18

28

<223> Growth factor and cytokines receptors family.

<400> 22
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Met Leu Leu Leu Thr Leu Leu Leu Leu Leu Leu Leu Leu Lys Gly
 1               5                  10                  15

Ser Cys Leu Glu Trp Gly Leu Val Gly Ala Gln Lys Val Ser Ser
               20                  25                  30

Ala Thr Asp Ala Pro Ile Arg Asp Trp Ala Phe Phe Pro Pro Ser
               35                  40                  45

Phe Leu Cys Leu Leu Pro His Arg Pro Ala Met Thr Cys Ser Gln
               50                  55                  60

Ala Gln Pro Arg Gly Glu Gly Glu Lys Val Gly Asp Gly
               65                  70
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<210> 23
<211> 2883
<212> DNA
<213> Homo sapiens

<400> 23
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cagcggacaa aggagcatgt ccgcgccggg gaaggcccgt cctccggccg 100
ccataaggct ccggtcgccg ctgggcccgc gccgcgctcc tgcccgcccg 150
ggctccgggg cggcccgcta ggccagtgcg ccgccgctcg ccccgcaggc 200
cccggcccgc agcatggagc cacccggacg ccggcggggc cgcgcgcagc 250
cgccgctgtt gctgccgctc tcgctgttag cgctgctcgc gctgctggga 300
ggcggcggcg gcggcggcgc cgcggcgctg cccgccggct gcaagcacga 350
tgggcggccc cgagggggctg gcagggcggc gggcgccgcc gagggcaagg 400
tggtgtgcag cagcctggaa ctcgcgcagg tcctgccccc agatactctg 450
cccaaccgca cggtcaccct gattctgagt aacaataaga tatccgagct 500
gaagaatggc tcattttctg ggttaagtct ccttgaaaga ttggacctcc 550
gaaacaatct tattagtagt atagatccag gtgccttctg gggactgtca 600
tctctaaaaa gattggatct gacaaacaat cgaataggat gtctgaatgc 650
agacatattt cgaggactca ccaatctggt tcggctaaac ctttcgggga 700
atttgttttc ttcattatct caaggaactt ttgattatct tgcgtcatta 750
cggtctttgg aattccagac tgagtatctt ttgtgtgact gtaacatact 800
gtggatgcat cgctgggtaa aggagaagaa catcacggta cgggatacca 850
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29

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ggtgtgttta tcctaagtca ctgcaggccc aaccagtcac aggcgtgaag 900

caggagctgt tgacatgcga ccctccgctt gaattgccgt ctttctacat 950

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agtgcatggc ttcatatatt gatcaggaca tgcaagtgtt gtggtatcag 1050

gatgggagaa tagttgaaac cgatgaatcg caaggtattt ttgttgaaaa 1100

gaacatgatt cacaactgct ccttgattgc aagtgcccta accatttcta 1150

atattcaggc tggatctact ggaaattggg gctgtcatgt ccagaccaaa 1200

cgtgggaata atacgaggac tgtggatatt gtggtattag agagttctgc 1250

acagtactgt cctccagaga gggtggtaaa caacaaaggt gacttcagat 1300

ggcccagaac attggcaggc attactgcat atctgcagtg tacgcggaac 1350

acccatggca gtgggatata tcccggaaac ccacaggatg agagaaaagc 1400

ttggcgcaga tgtgatagag gtggctttg ggcagatgat gattattctc 1450

gctgtcagta tgcaaatgat gtcactagag ttctttatat gtttaatcag 1500

atgcccctca atcttaccaa tgccgtggca acagctcgac agttactggc 1550

ttacactgtg gaagcagcca acttttctga caaatggat gttatatttg 1600

tggcagaaat gattgaaaaa tttggaagat ttaccaagga ggaaaaatca 1650

aaagagctag gtgacgtgat ggttgacatt gcaagtaaca tcatgttggc 1700

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tggcagcctc tgatcgtaca ggactttcgg attatgggag gcgggatcca 1950

gagggaaacc tggataagca gctgagcttt aagtgcaatg tttcaaatac 2000

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ctatttacag ttaaattaga atgctccaaa tgttctgctt cgcaaaataa 2100

ccttattaaa agattttttt ttgcaggaag ataggtatta ttgcttttgc 2150

tactgtttta aagaaaacta accaggaaga actgcattac gactttcaag 2200

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gaaattacat tttataactg cagtggtata aatgcaaata tactattgtt 2300
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30

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acatgtgaaa aaatttttatt tgacttaaaa gtttatttat ttgttttttt 2350

gctcctgatt ttaagacaat aagatgtttt catgggcccc taaaagtatc 2400

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tcaataatat cacaaacaat attccagtca ttttaatggc tgcataataa 2800

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<210> 24
<211> 616
<212> PRT
<213> Homo sapiens

<220>
<221> sig_peptide
<222> 1-33
<223> Signal peptide.

<220>
<221> TRANSMEM
<222> 13-40
<223> Transmembrane domain (type II).

<400> 24
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Met Glu Pro Pro Gly Arg Arg Arg Gly Arg Ala Gln Pro Pro Leu
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Leu Leu Pro Leu Ser Leu Leu Ala Leu Leu Ala Leu Leu Gly Gly
                20                  25                  30

Gly Gly Gly Gly Gly Ala Ala Ala Leu Pro Ala Gly Cys Lys His
                35                  40                  45

Asp Gly Arg Pro Arg Gly Ala Gly Arg Ala Ala Gly Ala Ala Glu
                50                  55                  60

Gly Lys Val Val Cys Ser Ser Leu Glu Leu Ala Gln Val Leu Pro
                65                  70                  75

Pro Asp Thr Leu Pro Asn Arg Thr Val Thr Leu Ile Leu Ser Asn
                80                  85                  90
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31

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Asn Lys Ile Ser Glu Leu Lys Asn Gly Ser Phe Ser Gly Leu Ser
                95                    100                   105

Leu Leu Glu Arg Leu Asp Leu Arg Asn Asn Leu Ile Ser Ser Ile
                110                   115                   120

Asp Pro Gly Ala Phe Trp Gly Leu Ser Ser Leu Lys Arg Leu Asp
                125                   130                   135

Leu Thr Asn Asn Arg Ile Gly Cys Leu Asn Ala Asp Ile Phe Arg
                140                   145                   150

Gly Leu Thr Asn Leu Val Arg Leu Asn Leu Ser Gly Asn Leu Phe
                155                   160                   165

Ser Ser Leu Ser Gln Gly Thr Phe Asp Tyr Leu Ala Ser Leu Arg
                170                   175                   180

Ser Leu Glu Phe Gln Thr Glu Tyr Leu Leu Cys Asp Cys Asn Ile
                185                   190                   195

Leu Trp Met His Arg Trp Val Lys Glu Lys Asn Ile Thr Val Arg
                200                   205                   210

Asp Thr Arg Cys Val Tyr Pro Lys Ser Leu Gln Ala Gln Pro Val
                215                   220                   225

Thr Gly Val Lys Gln Glu Leu Leu Thr Cys Asp Pro Pro Leu Glu
                230                   235                   240

Leu Pro Ser Phe Tyr Met Thr Pro Ser His Arg Gln Val Val Phe
                245                   250                   255

Glu Gly Asp Ser Leu Pro Phe Gln Cys Met Ala Ser Tyr Ile Asp
                260                   265                   270

Gln Asp Met Gln Val Leu Trp Tyr Gln Asp Gly Arg Ile Val Glu
                275                   280                   285

Thr Asp Glu Ser Gln Gly Ile Phe Val Glu Lys Asn Met Ile His
                290                   295                   300

Asn Cys Ser Leu Ile Ala Ser Ala Leu Thr Ile Ser Asn Ile Gln
                305                   310                   315

Ala Gly Ser Thr Gly Asn Trp Gly Cys His Val Gln Thr Lys Arg
                320                   325                   330

Gly Asn Asn Thr Arg Thr Val Asp Ile Val Val Leu Glu Ser Ser
                335                   340                   345

Ala Gln Tyr Cys Pro Pro Glu Arg Val Val Asn Asn Lys Gly Asp
                350                   355                   360

Phe Arg Trp Pro Arg Thr Leu Ala Gly Ile Thr Ala Tyr Leu Gln
                365                   370                   375

Cys Thr Arg Asn Thr His Gly Ser Gly Ile Tyr Pro Gly Asn Pro
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Gln Asp Glu Arg Lys Ala Trp Arg Arg Cys Asp Arg Gly Gly Phe
                395   400   405

Trp Ala Asp Asp Asp Tyr Ser Arg Cys Gln Tyr Ala Asn Asp Val
                410   415   420

Thr Arg Val Leu Tyr Met Phe Asn Gln Met Pro Leu Asn Leu Thr
                425   430   435

Asn Ala Val Ala Thr Ala Arg Gln Leu Leu Ala Tyr Thr Val Glu
                440   445   450

Ala Ala Asn Phe Ser Asp Lys Met Asp Val Ile Phe Val Ala Glu
                455   460   465

Met Ile Glu Lys Phe Gly Arg Phe Thr Lys Glu Glu Lys Ser Lys
                470   475   480

Glu Leu Gly Asp Val Met Val Asp Ile Ala Ser Asn Ile Met Leu
                485   490   495

Ala Asp Glu Arg Val Leu Trp Leu Ala Gln Arg Glu Ala Lys Ala
                500   505   510

Cys Ser Arg Ile Val Gln Cys Leu Gln Arg Ile Ala Thr Tyr Arg
                515   520   525

Leu Ala Gly Gly Ala His Val Tyr Ser Thr Tyr Ser Pro Asn Ile
                530   535   540

Ala Leu Glu Ala Tyr Val Ile Lys Ser Thr Gly Phe Thr Gly Met
                545   550   555

Thr Cys Thr Val Phe Gln Lys Val Ala Ala Ser Asp Arg Thr Gly
                560   565   570

Leu Ser Asp Tyr Gly Arg Arg Asp Pro Glu Gly Asn Leu Asp Lys
                575   580   585

Gln Leu Ser Phe Lys Cys Asn Val Ser Asn Thr Phe Ser Ser Leu
                590   595   600

Ala Leu Lys Val Cys Tyr Ile Leu Gln Ser Phe Lys Thr Ile Tyr
                605   610   615

Ser

<210> 25
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24

<223> Synthetic construct

<400> 25
 gaggactcac caatctggtt cggc 24

<210> 26
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 26
 aactggaaag gaaggctgtc tccc 24

<210> 27
<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 27
 gtaaaggaga agaacatcac ggtacgggat accaggtgtg tttatcctaa 50

<210> 28
<211> 683
<212> DNA
<213> Homo sapiens

<400> 28
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 ctgacggcgg ccacagtggc cggcgtacat gtgaagcagc agtgggacca 100

 gcagaggctt cgtgacggag ttatcagaga cattgagagg caaattcgga 150

 aaaaagaaaa cattcgtctt ttgggagaac agattatttt gactgagcaa 200

 cttgaagcag aaagagagaa gatgttattg gcaaaggat ctcaaaaatc 250

 atgacttgaa tgtgaaatat ctgttggaca gacaacacga gtttgtgtgt 300

 gtgtgttgat ggagagtagc ttagtagtat cttcatcttt ttttttggtc 350

 actgtccttt taaacttgat caaataaagg acagtgggtc atataagtta 400

 ctgctttcag ggtcccttat atctgaataa aggagtgtgg gcagacactt 450

 tttggaagag tctgtctggg tgatcctggt agaagcccca ttagggtcac 500

 tgtccagtgc ttagggttgt tactgagaag cactgccgag cttgtgagaa 550

34

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atgacgaagc cacgagaaca tcgacctcag aaggactgga ggaaggtgaa 650

gtggagggag agacgctcct gatcgtcgaa tcc 683

<210> 29
<211> 81
<212> PRT
<213> Homo sapiens

<220>
<221> sig_peptide
<222> 1-21
<223> Signal peptide.

<400> 29
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1   5   10   15

Thr Ala Ala Thr Val Ala Gly Val His Val Lys Gln Gln Trp Asp
                20   25   30

Gln Gln Arg Leu Arg Asp Gly Val Ile Arg Asp Ile Glu Arg Gln
                35   40   45

Ile Arg Lys Lys Glu Asn Ile Arg Leu Leu Gly Glu Gln Ile Ile
                50   55   60

Leu Thr Glu Gln Leu Glu Ala Glu Arg Glu Lys Met Leu Leu Ala
                65   70   75

Lys Gly Ser Gln Lys Ser
                80

<210> 30
<211> 2128
<212> DNA
<213> Homo sapiens

<400> 30
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tccgtggatt cctctgctaa gaccgctgcc atgccagtga cggtaacccg 150

caccaccatc acaaccacca cgacgtcatc ttcgggcctg gggtccccca 200

tgatcgtggg gtcccctcgg gccctgacac agcccctggg tctccttcgc 250

ctgctgcagc tggtgtctac ctgcgtggcc ttctcgctgg tggctagcgt 300

gggcgcctgg acggggtcca tgggcaactg gtccatgttc acctggtgct 350

tctgcttctc cgtgaccctg atcatcctca tcgtggagct gtgcgggctc 400

caggcccgct tccccctgtc ttggcgcaac ttccccatca ccttcgcctg 450

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accttcttct cctgcatcgc gtgtgtggct tacgccaccg aagtggcctg 600

gacccgggcc cggcccggcg agatcactgg ctatatggcc accgtacccg 650

ggctgctgaa ggtgctggag accttcgttg cctgcatcat cttcgcgttc 700

atcagcgacc ccaacctgta ccagcaccag ccggccctgg agtggtgcgt 750

ggcggtgtac gccatctgct tcatcctagc ggccatcgcc atcctgctga 800

acctggggga gtgcaccaac gtgctaccca tccccttccc cagcttcctg 850

tcggggctgg ccttgctgtc tgtcctcctc tatgccaccg cccttgttct 900

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gaccgccgac tggctgtggc catcctgacg gccatcaacc tactggcgta 1050

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gtgtgtgtgt gtgtgtgttt gggggggtggg gggtgggtag ctggggattg 1850

ggccctcttt ctcccagtgg aggaaggtgt gcagtgtact tcccctttaa 1900
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36

attaaaaaac atatatatat atatatttgg aggtcagtaa tttccaatgg 1950

gcgggaggca ttaagcaccg accctgggtc cctaggcccc gcctggcact 2000

cagccttgcc agagattggc tccagaattt ttgccaggct tacagaacac 2050

ccactgccta gaggccatct taaaggaagc aggggctgga tgcctttcat 2100

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<210> 31
<211> 322
<212> PRT
<213> Homo sapiens

<400> 31

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Met Pro Val Thr Val Thr Arg Thr Thr Ile Thr Thr Thr Thr Thr
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Ser Ser Ser Gly Leu Gly Ser Pro Met Ile Val Gly Ser Pro Arg
                20                  25                  30

Ala Leu Thr Gln Pro Leu Gly Leu Leu Arg Leu Leu Gln Leu Val
                35                  40                  45

Ser Thr Cys Val Ala Phe Ser Leu Val Ala Ser Val Gly Ala Trp
                50                  55                  60

Thr Gly Ser Met Gly Asn Trp Ser Met Phe Thr Trp Cys Phe Cys
                65                  70                  75

Phe Ser Val Thr Leu Ile Ile Leu Ile Val Glu Leu Cys Gly Leu
                80                  85                  90

Gln Ala Arg Phe Pro Leu Ser Trp Arg Asn Phe Pro Ile Thr Phe
                95                  100                 105

Ala Cys Tyr Ala Ala Leu Phe Cys Leu Ser Ala Ser Ile Ile Tyr
                110                 115                 120

Pro Thr Thr Tyr Val Gln Phe Leu Ser His Gly Arg Ser Arg Asp
                125                 130                 135

His Ala Ile Ala Ala Thr Phe Phe Ser Cys Ile Ala Cys Val Ala
                140                 145                 150

Tyr Ala Thr Glu Val Ala Trp Thr Arg Ala Arg Pro Gly Glu Ile
                155                 160                 165

Thr Gly Tyr Met Ala Thr Val Pro Gly Leu Leu Lys Val Leu Glu
                170                 175                 180

Thr Phe Val Ala Cys Ile Ile Phe Ala Phe Ile Ser Asp Pro Asn
                185                 190                 195

Leu Tyr Gln His Gln Pro Ala Leu Glu Trp Cys Val Ala Val Tyr
                200                 205                 210
```

Ala Ile Cys Phe Ile Leu Ala Ala Ile Ala Ile Leu Leu Asn Leu
                215   220   225

Gly Glu Cys Thr Asn Val Leu Pro Ile Pro Phe Pro Ser Phe Leu
                230   235   240

Ser Gly Leu Ala Leu Leu Ser Val Leu Leu Tyr Ala Thr Ala Leu
                245   250   255

Val Leu Trp Pro Leu Tyr Gln Phe Asp Glu Lys Tyr Gly Gly Gln
                260   265   270

Pro Arg Arg Ser Arg Asp Val Ser Cys Ser Arg Ser His Ala Tyr
                275   280   285

Tyr Val Cys Ala Trp Asp Arg Arg Leu Ala Val Ala Ile Leu Thr
                290   295   300

Ala Ile Asn Leu Leu Ala Tyr Val Ala Asp Leu Val His Ser Ala
                305   310   315

His Leu Val Phe Val Lys Val
                320

<210> 32
<211> 3680
<212> DNA
<213> Homo sapiens

<400> 32
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ctggccagcc tatgcatttt taagaaatta ttctgtatta ggtgctgtgc   200

taaacattgg gcactacagt gaccaaaaca gactgaattc cccaagagcc   250

aaagaccagt gagggagacc aacaagaaac aggaaatgca aaagagacca   300

ttattactca ctatgactaa gggtcacaaa tggggtacgt tgatggagag   350

tgatttgtta agagactaca gagggaggac agactaccaa gagggggcc   400

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gaaagagcta gccagccatc agaatagtcc agaagagatg gggagcacta   500

cactcactac actttggcct gagaaaatag catgggattg gaggaggctg   550

ggggaacacc acttctgccg acctgggcag gaggcattga gggcttgaga   600

aagggcaatg gcagtagcag tagaaaggac agggtaggag cagggacttt   650

gcaggtggaa tcattaggtc ttatcaacag atatgggcaa gcaaagccag   700

38

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gggagaattg atggtaatgc tgaggtttgg agccaggcta gatgggacag 750

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atgggaagac caagaggagg agcaaggggc agaggggaag ggaatcttaa 900

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39

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taatataaaa atctttgtaa atctctaaaa 3680

<210> 33
<211> 335
<212> PRT
<213> Homo sapiens

<400> 33
Met Phe Leu Ala Thr Leu Ser Phe Leu Leu Pro Phe Ala His Pro
1   5   10   15

Phe Gly Thr Val Ser Cys Glu Tyr Met Leu Gly Ser Pro Leu Ser
                20   25   30

Ser Leu Ala Gln Val Asn Leu Ser Pro Phe Ser His Pro Lys Val
                35   40   45

His Met Asp Pro Asn Tyr Cys His Pro Ser Thr Ser Leu His Leu
                50   55   60

Cys Ser Leu Ala Trp Ser Phe Thr Arg Leu Leu His Pro Pro Leu
                65   70   75

Ser Pro Gly Ile Ser Gln Val Val Lys Asp His Val Thr Lys Pro
                80   85   90

Thr Ala Met Ala Gln Gly Arg Val Ala His Leu Ile Glu Trp Lys
                95   100   105

Gly Trp Ser Lys Pro Ser Asp Ser Pro Ala Ala Leu Glu Ser Ala
                110   115   120

Phe Ser Ser Tyr Ser Asp Leu Ser Glu Gly Glu Gln Glu Ala Arg
                125   130   135

Phe Ala Ala Gly Val Ala Glu Gln Phe Ala Ile Ala Glu Ala Lys
                140   145   150

Leu Arg Ala Trp Ser Ser Val Asp Gly Glu Asp Ser Thr Asp Asp
                155   160   165

Ser Tyr Asp Glu Asp Phe Ala Gly Gly Met Asp Thr Asp Met Ala
                170   175   180

Gly Gln Leu Pro Leu Gly Pro His Leu Gln Asp Leu Phe Thr Gly
                185   190   195

His Arg Phe Ser Arg Pro Val Arg Gln Gly Ser Val Glu Pro Glu
                200   205   210

Ser Asp Cys Ser Gln Thr Val Ser Pro Asp Thr Leu Cys Ser Ser
                215   220   225

Leu Cys Ser Leu Glu Asp Gly Leu Leu Gly Ser Pro Ala Arg Leu
                230   235   240

41

```
Ala Ser Gln Leu Leu Gly Asp Glu Leu Leu Leu Ala Lys Leu Pro
            245               250               255

Pro Ser Arg Glu Ser Ala Phe Arg Ser Leu Gly Pro Leu Glu Ala
            260               265               270

Gln Asp Ser Leu Tyr Asn Ser Pro Leu Thr Glu Ser Cys Leu Ser
            275               280               285

Pro Ala Glu Glu Glu Pro Ala Pro Cys Lys Asp Cys Gln Pro Leu
            290               295               300

Cys Pro Pro Leu Thr Gly Ser Trp Glu Arg Gln Arg Gln Ala Ser
            305               310               315

Asp Leu Ala Ser Ser Gly Val Val Ser Leu Asp Glu Asp Glu Ala
            320               325               330

Glu Pro Glu Glu Gln
            335
```

```
<210> 34
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-25
<223> Synthetic construct

<400> 34
 tgtcctttgt cccagacttc tgtcc                                25

<210> 35
<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 35
 ctggatgcta atgtgtccag taaatgatcc ccttatcccg tcgcgatgct        50

<210> 36
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-25
<223> Synthetic construct.

<400> 36
```

```
     ttccactcaa tgaggtgagc cactc 25

<210> 37
<211> 23
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-23
<223> Synthetic construct.

<400> 37
 ggcgagccct aactatccag gag 23

<210> 38
<211> 39
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-39
<223> Synthetic construct.

<400> 38
 ggagatcgct gcgctggcca ggtcctccct gcatggtat 39

<210> 39
<211> 22
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-22
<223> Synthetic construct.

<400> 39
 ctgctgcaaa gcgagcctct tg 22

<210> 40
<211> 2084
<212> DNA
<213> Homo sapiens

<400> 40
 ggttcctggg cgctctgtta cacaagcaag atacagccag ccccacctaa 50

 ttttgtttcc ctggcaccct cctgctcagt gcgacattgt cacacttaac 100

 ccatctgttt tctctaatgc acgacagatt cctttcagac aggacaactg 150

 tgatatttca gttcctgatt gtaaatacct cctaagcctg aagcttctgt 200

 tactagccat tgtgagcttc agtttcttca tctgcaaaat gggcataata 250

 caatctattc ttgccacatc aagggattgt tattccttta aaaaaaaacc 300
```

43

```
aataccaaag aagcctacaa tgttggcctt agccaaaatt ctgttgattt 350

caacgttgtt ttattcactt ctatcgggga gccatggaaa agaaaatcaa 400

gacataaaca caacacagaa cattgcagaa gtttttaaaa caatggaaaa 450

taaacctatt tctttggaaa gtgaagcaaa cttaaactca gataaagaaa 500

atataaccac ctcaaatctc aaggcgagtc attccctcc tttgaatcta 550

cccaacaaca gccacggaat aacagatttc tccagtaact catcagcaga 600

gcattctttg ggcagtctaa aacccacatc taccatttcc acaagccctc 650

ccttgatcca tagctttgtt tctaaagtgc cttggaatgc acctatagca 700

gatgaagatc ttttgcccat ctcagcacat cccaatgcta cacctgctct 750

gtcttcagaa aacttcactt ggtctttggt caatgacacc gtgaaaactc 800

ctgataacag ttccattaca gttagcatcc tctcttcaga accaacttct 850

ccatctgtga ccccctttgat agtggaacca agtggatggc ttaccacaaa 900

cagtgatagc ttcactgggt ttaccccctta tcaagaaaaa acaactctac 950

agcctacctt aaaattcacc aataattcaa aactctttcc aaatacgtca 1000

gatccccaaa aagaaaatag aaatacagga atagtattcg gggccatttt 1050

aggtgctatt ctgggtgtct cattgcttac tcttgtgggc tacttgttgt 1100

gtggaaaaag gaaaacggat tcattttccc atcggcgact ttatgacgac 1150

agaaatgaac cagttctgcg attagacaat gcaccggaac cttatgatgt 1200

gagttttggg aattctagct actacaatcc aactttgaat gattcagcca 1250

tgccagaaag tgaagaaaat gcacgtgatg gcattcctat ggatgacata 1300

cctccacttc gtacttctgt atagaactaa cagcaaaaag gcgttaaaca 1350

gcaagtgtca tctacatcct agccttttga caaattcatc tttcaaaagg 1400

ttacacaaaa ttactgtcac gtggattttg tcaaggagaa tcataaaagc 1450

aggagaccag tagcagaaat gtagacagga tgtatcatcc aaaggttttc 1500

tttcttacaa tttttggcca tcctgaggca tttactaagt agccttaatt 1550

tgtattttag tagtattttc ttagtagaaa atatttgtgg aatcagataa 1600

aactaaaaga tttcaccatt acagccctgc ctcataacta aataataaaa 1650

attattccac caaaaaattc taaaacaatg aagatgactc tttactgctc 1700

tgcctgaagc cctagtacca taattcaaga ttgcattttc ttaaatgaaa 1750
```

44

```
attgaaaggg tgctttttaa agaaaatttg acttaaagct aaaaagagga 1800

catagcccag agtttctgtt attgggaaat tgaggcaata gaaatgacag 1850

acctgtattc tagtacgtta taattttcta gatcagcaca cacatgatca 1900

gcccactgag ttatgaagct gacaatgact gcattcaacg gggccatggc 1950

aggaaagctg accctaccca ggaaagtaat agcttcttta aaagtcttca 2000

aaggttttgg gaattttaac ttgtcttaat atatcttagg cttcaattat 2050

ttgggtgcct taaaaactca atgagaatca tggt 2084
```

<210> 41
<211> 334
<212> PRT
<213> Homo sapiens

<400> 41

```
Met Leu Ala Leu Ala Lys Ile Leu Leu Ile Ser Thr Leu Phe Tyr
 1               5                  10                  15

Ser Leu Leu Ser Gly Ser His Gly Lys Glu Asn Gln Asp Ile Asn
            20                  25                  30

Thr Thr Gln Asn Ile Ala Glu Val Phe Lys Thr Met Glu Asn Lys
            35                  40                  45

Pro Ile Ser Leu Glu Ser Glu Ala Asn Leu Asn Ser Asp Lys Glu
            50                  55                  60

Asn Ile Thr Thr Ser Asn Leu Lys Ala Ser His Ser Pro Pro Leu
            65                  70                  75

Asn Leu Pro Asn Asn Ser His Gly Ile Thr Asp Phe Ser Ser Asn
            80                  85                  90

Ser Ser Ala Glu His Ser Leu Gly Ser Leu Lys Pro Thr Ser Thr
            95                 100                 105

Ile Ser Thr Ser Pro Pro Leu Ile His Ser Phe Val Ser Lys Val
           110                 115                 120

Pro Trp Asn Ala Pro Ile Ala Asp Glu Asp Leu Leu Pro Ile Ser
           125                 130                 135

Ala His Pro Asn Ala Thr Pro Ala Leu Ser Ser Glu Asn Phe Thr
           140                 145                 150

Trp Ser Leu Val Asn Asp Thr Val Lys Thr Pro Asp Asn Ser Ser
           155                 160                 165

Ile Thr Val Ser Ile Leu Ser Ser Glu Pro Thr Ser Pro Ser Val
           170                 175                 180

Thr Pro Leu Ile Val Glu Pro Ser Gly Trp Leu Thr Thr Asn Ser
           185                 190                 195
```

45

Asp Ser Phe Thr Gly Phe Thr Pro Tyr Gln Glu Lys Thr Thr Leu
            200   205   210

Gln Pro Thr Leu Lys Phe Thr Asn Asn Ser Lys Leu Phe Pro Asn
            215   220   225

Thr Ser Asp Pro Gln Lys Glu Asn Arg Asn Thr Gly Ile Val Phe
            230   235   240

Gly Ala Ile Leu Gly Ala Ile Leu Gly Val Ser Leu Leu Thr Leu
            245   250   255

Val Gly Tyr Leu Leu Cys Gly Lys Arg Lys Thr Asp Ser Phe Ser
            260   265   270

His Arg Arg Leu Tyr Asp Asp Arg Asn Glu Pro Val Leu Arg Leu
            275   280   285

Asp Asn Ala Pro Glu Pro Tyr Asp Val Ser Phe Gly Asn Ser Ser
            290   295   300

Tyr Tyr Asn Pro Thr Leu Asn Asp Ser Ala Met Pro Glu Ser Glu
            305   310   315

Glu Asn Ala Arg Asp Gly Ile Pro Met Asp Asp Ile Pro Pro Leu
            320   325   330

Arg Thr Ser Val

<210> 42
<211> 1594
<212> DNA
<213> Homo sapiens

<400> 42
aacaggatct cctcttgcag tctgcagccc aggacgctga ttccagcagc 50

gccttaccgc gcagcccgaa gattcactat ggtgaaaatc gccttcaata 100

cccctaccgc cgtgcaaaag gaggaggcgc ggcaagacgt ggaggccctc 150

ctgagccgca cggtcagaac tcagatactg accggcaagg agctccgagt 200

tgccacccag gaaaaagagg gctcctctgg gagatgtatg cttactctct 250

taggcctttc attcatcttg gcaggactta ttgttggtgg agcctgcatt 300

tacaagtact tcatgcccaa gagcaccatt taccgtggag agatgtgctt 350

ttttgattct gaggatcctg caaattccct tcgtggagga gagcctaact 400

tcctgcctgt gactgaggag gctgacattc gtgaggatga caacattgca 450

atcattgatg tgcctgtccc cagtttctct gatagtgacc ctgcagcaat 500

tattcatgac tttgaaaagg gaatgactgc ttacctggac ttgttgctgg 550

46

ggaactgcta tctgatgccc ctcaatactt ctattgttat gcctccaaaa 600

aatctggtag agctctttgg caaactggcg agtggcagat atctgcctca 650

aacttatgtg gttcgagaag acctagttgc tgtggaggaa attcgtgatg 700

ttagtaacct tggcatcttt atttaccaac tttgcaataa cagaaagtcc 750

ttccgccttc gtcgcagaga cctcttgctg ggtttcaaca aacgtgccat 800

tgataaatgc tggaagatta gacacttccc caacgaattt attgttgaga 850

ccaagatctg tcaagagtaa gaggcaacag atagagtgtc cttggtaata 900

agaagtcaga gatttacaat atgactttaa cattaaggtt tatgggatac 950

tcaagatatt tactcatgca tttactctat tgcttatgct ttaaaaaaag 1000

gaaaaaaaaa aaaactacta accactgcaa gctcttgtca aattttagtt 1050

taattggcat tgcttgtttt ttgaaactga aattacatga gtttcatttt 1100

ttctttgcat ttatagggtt tagatttctg aaagcagcat gaatatatca 1150

cctaacatcc tgacaataaa ttccatccgt tgtttttttt gtttgtttgt 1200

tttttctttt cctttaagta agctctttat tcatcttatg gtggagcaat 1250

tttaaaattt gaaatatttt aaattgtttt tgaacttttt gtgtaaaata 1300

tatcagatct caacattgtt ggtttctttt gtttttcatt ttgtacaact 1350

ttcttgaatt tagaaattac atctttgcag ttctgttagg tgctctgtaa 1400

ttaacctgac ttatatgtga acaattttca tgagacagtc atttttaact 1450

aatgcagtga ttctttctca ctactatctg tattgtggaa tgcacaaaat 1500

tgtgtaggtg ctgaatgctg taaggagttt aggttgtatg aattctacaa 1550

ccctataata aattttactc tatacaaaaa aaaaaaaaa aaaa 1594

<210> 43
<211> 263
<212> PRT
<213> Homo sapiens

<400> 43
 Met Val Lys Ile Ala Phe Asn Thr Pro Thr Ala Val Gln Lys Glu
  1   5   10   15

 Glu Ala Arg Gln Asp Val Glu Ala Leu Leu Ser Arg Thr Val Arg
                 20   25   30

 Thr Gln Ile Leu Thr Gly Lys Glu Leu Arg Val Ala Thr Gln Glu
                     35   40   45

 Lys Glu Gly Ser Ser Gly Arg Cys Met Leu Thr Leu Leu Gly Leu

47

```
Ser Phe Ile Leu Ala Gly Leu Ile Val Gly Gly Ala Cys Ile Tyr
                65                        70                        75

Lys Tyr Phe Met Pro Lys Ser Thr Ile Tyr Arg Gly Glu Met Cys
                80                        85                        90

Phe Phe Asp Ser Glu Asp Pro Ala Asn Ser Leu Arg Gly Gly Glu
                95                        100                       105

Pro Asn Phe Leu Pro Val Thr Glu Glu Ala Asp Ile Arg Glu Asp
                110                       115                       120

Asp Asn Ile Ala Ile Ile Asp Val Pro Val Pro Ser Phe Ser Asp
                125                       130                       135

Ser Asp Pro Ala Ala Ile Ile His Asp Phe Glu Lys Gly Met Thr
                140                       145                       150

Ala Tyr Leu Asp Leu Leu Leu Gly Asn Cys Tyr Leu Met Pro Leu
                155                       160                       165

Asn Thr Ser Ile Val Met Pro Pro Lys Asn Leu Val Glu Leu Phe
                170                       175                       180

Gly Lys Leu Ala Ser Gly Arg Tyr Leu Pro Gln Thr Tyr Val Val
                185                       190                       195

Arg Glu Asp Leu Val Ala Val Glu Glu Ile Arg Asp Val Ser Asn
                200                       205                       210

Leu Gly Ile Phe Ile Tyr Gln Leu Cys Asn Asn Arg Lys Ser Phe
                215                       220                       225

Arg Leu Arg Arg Arg Asp Leu Leu Leu Gly Phe Asn Lys Arg Ala
                230                       235                       240

Ile Asp Lys Cys Trp Lys Ile Arg His Phe Pro Asn Glu Phe Ile
                245                       250                       255

Val Glu Thr Lys Ile Cys Gln Glu
                260
```

<210> 44
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-24
<223> Synthetic construct.

<400> 44
 gaaagacacg acacagcagc ttgc 24

<210> 45

```
<211> 20
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-20
<223> Synthetic construct.

<400> 45
 gggaactgct atctgatgcc 20

<210> 46
<211> 26
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-26
<223> Synthetic construct.

<400> 46
 caggatctcc tcttgcagtc tgcagc 26

<210> 47
<211> 28
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-28
<223> Synthetic construct.

<400> 47
 cttctcgaac cacataagtt tgaggcag 28

<210> 48
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-25
<223> Synthetic construct.

<400> 48
 cacgattccc tccacagcaa ctggg 25

<210> 49
<211> 1969
<212> DNA
<213> Homo sapiens

<400> 49
 ggaggaggga gggcgggcag gcgccagccc agagcagccc cgggcaccag 50
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```
cacggactct ctcttccagc ccaggtgccc cccactctcg ctccattcgg 100

cgggagcacc cagtcctgta cgccaaggaa ctggtcctgg gggcaccatg 150

gtttcggcgg cagcccccag cctcctcatc cttctgttgc tgctgctggg 200

gtctgtgcct gctaccgacg cccgctctgt gcccctgaag gccacgttcc 250

tggaggatgt ggcgggtagt ggggaggccg agggctcgtc ggcctcctcc 300

ccgagcctcc cgccaccctg accccggcc ctcagcccca catcgatggg 350

gccccagccc acaaccctgg ggggcccatc accccccacc aacttcctgg 400

atgggatagt ggacttcttc cgccagtacg tgatgctgat tgctgtggtg 450

ggctccctgg cctttctgct gatgttcatc gtctgtgccg cggtcatcac 500

ccggcagaag cagaaggcct cggcctatta cccatcgtcc ttccccaaga 550

agaagtacgt ggaccagagt gaccgggccg ggggcccccg ggccttcagt 600

gaggtccccg acagagcccc cgacagcagg cccgaggaag ccctggattc 650

ctcccggcag ctccaggccg acatcttggc cgccacccag aacctcaagt 700

cccccaccag ggctgcactg ggcggtgggg acggagccag gatggtggag 750

ggcaggggcg cagaggaaga ggagaagggc agccaggagg gggaccagga 800

agtccaggga catggggtcc cagtggagac accagaggcg caggaggagc 850

cgtgctcagg ggtccttgag ggggctgtgg tggccggtga gggccaaggg 900

gagctggaag ggtctctctt gttagcccag gaagcccagg accagtggg 950

tccccccgaa agccctgtg cttgcagcag tgtccacccc agtgtctaac 1000

agtcctcccg ggctgccagc cctgactgtc gggcccccaa gtggtcacct 1050

ccccgtgtat gaaaaggcct tcagccctga ctgcttcctg acactccctc 1100

cttggcctcc ctgtggtgcc aatcccagca tgtgctgatt ctacagcagg 1150

cagaaatgct ggtccccggt gccccggagg aatcttacca agtgccatca 1200

tccttcacct cagcagcccc aaagggctac atcctacagc acagctcccc 1250

tgacaaagtg agggagggca cgtgtccctg tgacagccag gataaaacat 1300

cccccaaagt gctgggatta caggcgtgag ccaccgtgcc cggcccaaac 1350

tacttttaa aacagctaca gggtaaaatc ctgcagcacc cactctggaa 1400

aatactgctc ttaattttcc tgaaggtggc cccctgtttc tagttggtcc 1450

aggattaggg atgtggggta tagggcattt aaatcctctc aagcgctctc 1500
```

50

caagcacccc cggcctgggg gtgagtttct catcccgcta ctgctgctgg 1550

gatcaggttg aatgaatgga actcttcctg tctggcctcc aaagcagcct 1600

agaagctgag gggctgtgtt tgaggggacc tccaccctgg ggaagtccga 1650

ggggctgggg aagggtttct gacgcccagc ctggagcagg ggggccctgg 1700

ccaccccctg ttgctcacac attgtctggc agcctgtgtc cacaatattc 1750

gtcagtcctc gacagggagc ctgggctccg tcctgcttta gggaggctct 1800

ggcaggaggt cctctccccc atccctccat ctggggctcc cccaacctct 1850

gcacagctct ccaggtgctg agatataatg caccagcaca ataaaccttt 1900

attccggcct gaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1950

aaaaaaaaaa aaaaaaaga 1969

<210> 50
<211> 283
<212> PRT
<213> Homo sapiens

<400> 50
```
Met Val Ser Ala Ala Ala Pro Ser Leu Leu Ile Leu Leu Leu Leu
 1               5                  10                  15

Leu Leu Gly Ser Val Pro Ala Thr Asp Ala Arg Ser Val Pro Leu
              20                  25                  30

Lys Ala Thr Phe Leu Glu Asp Val Ala Gly Ser Gly Glu Ala Glu
              35                  40                  45

Gly Ser Ser Ala Ser Ser Pro Ser Leu Pro Pro Pro Trp Thr Pro
              50                  55                  60

Ala Leu Ser Pro Thr Ser Met Gly Pro Gln Pro Thr Thr Leu Gly
              65                  70                  75

Gly Pro Ser Pro Pro Thr Asn Phe Leu Asp Gly Ile Val Asp Phe
              80                  85                  90

Phe Arg Gln Tyr Val Met Leu Ile Ala Val Val Gly Ser Leu Ala
              95                 100                 105

Phe Leu Leu Met Phe Ile Val Cys Ala Ala Val Ile Thr Arg Gln
             110                 115                 120

Lys Gln Lys Ala Ser Ala Tyr Tyr Pro Ser Ser Phe Pro Lys Lys
             125                 130                 135

Lys Tyr Val Asp Gln Ser Asp Arg Ala Gly Gly Pro Arg Ala Phe
             140                 145                 150

Ser Glu Val Pro Asp Arg Ala Pro Asp Ser Arg Pro Glu Glu Ala
             155                 160                 165
```

```
Leu Asp Ser Ser Arg Gln Leu Gln Ala Asp Ile Leu Ala Ala Thr
                170                 175                 180

Gln Asn Leu Lys Ser Pro Thr Arg Ala Ala Leu Gly Gly Gly Asp
                185                 190                 195

Gly Ala Arg Met Val Glu Gly Arg Gly Ala Glu Glu Glu Glu Lys
                200                 205                 210

Gly Ser Gln Glu Gly Asp Gln Glu Val Gln Gly His Gly Val Pro
                215                 220                 225

Val Glu Thr Pro Glu Ala Gln Glu Glu Pro Cys Ser Gly Val Leu
                230                 235                 240

Glu Gly Ala Val Val Ala Gly Glu Gly Gln Gly Glu Leu Glu Gly
                245                 250                 255

Ser Leu Leu Leu Ala Gln Glu Ala Gln Gly Pro Val Gly Pro Pro
                260                 265                 270

Glu Ser Pro Cys Ala Cys Ser Ser Val His Pro Ser Val
                275                 280
```

<210> 51
<211> 1734
<212> DNA
<213> Homo sapiens

<400> 51
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gtggactctg agaagcccag gcagttgagg acaggagaga gaaggctgca    50
gacccagagg gagggaggac agggagtcgg aaggaggagg acagaggagg   100
gcacagagac gcagagcaag ggcggcaagg aggagaccct ggtgggagga   150
agacactctg gagagagagg gggctgggca gagatgaagt tccaggggcc   200
cctggcctgc ctcctgctgg ccctctgcct gggcagtggg gaggctggcc   250
ccctgcagag cggagaggaa agcactggga caaatattgg ggaggccctt   300
ggacatggcc tgggagacgc cctgagcgaa ggggtgggaa aggccattgg   350
caaagaggcc ggaggggcag ctggctctaa agtcagtgag gcccttggcc   400
aagggaccag agaagcagtt ggcactggag tcaggcaggt tccaggcttt   450
ggcgcagcag atgctttggg caacagggtc ggggaagcag cccatgctct   500
gggaaacact gggcacgaga ttggcagaca ggcagaagat gtcattcgac   550
acggagcaga tgctgtccgc ggctcctggc agggggtgcc tggccacagt   600
ggtgcttggg aaacttctgg aggccatggc atctttggct ctcaaggtgg   650
ccttggaggc cagggccagg gcaatcctgg aggtctgggg actccgtggg   700
```

```
tccacggata ccccggaaac tcagcaggca gctttggaat gaatcctcag 750

ggagctccct ggggtcaagg aggcaatgga gggccaccaa actttgggac 800

caacactcag ggagctgtgg cccagcctgg ctatggttca gtgagagcca 850

gcaaccagaa tgaagggtgc acgaatcccc caccatctgg ctcaggtgga 900

ggctccagca actctggggg aggcagcggc tcacagtcgg gcagcagtgg 950

cagtggcagc aatggtgaca caacaatgg cagcagcagt ggtggcagca 1000

gcagtggcag cagcagtggc agcagcagtg gcggcagcag tggcggcagc 1050

agtggtggca gcagtggcaa cagtggtggc agcagaggtg acagcggcag 1100

tgagtcctcc tggggatcca gcaccggctc ctcctccggc aaccacggtg 1150

ggagcggcgg aggaaatgga cataaacccg ggtgtgaaaa gccagggaat 1200

gaagcccgcg ggagcgggga tctgggatt cagggcttca gaggacaggg 1250

agtttccagc aacatgaggg aaataagcaa agagggcaat cgcctccttg 1300

gaggctctgg agacaattat cggggggcaag ggtcgagctg gggcagtgga 1350

ggaggtgacg ctgttggtgg agtcaatact gtgaactctg agacgtctcc 1400

tgggatgttt aactttgaca ctttctggaa gaattttaaa tccaagctgg 1450

gtttcatcaa ctgggatgcc ataaacaagg accagagaag ctctcgcatc 1500

ccgtgacctc cagacaagga gccaccagat tggatgggag cccccacact 1550

ccctccttaa aacaccaccc tctcatcact aatctcagcc cttgcccttg 1600

aaataaacct tagctgcccc acaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1650

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1700

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1734
```

<210> 52
<211> 440
<212> PRT
<213> Homo sapiens

<400> 52

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 Met Lys Phe Gln Gly Pro Leu Ala Cys Leu Leu Leu Ala Leu Cys
  1               5                  10                  15

 Leu Gly Ser Gly Glu Ala Gly Pro Leu Gln Ser Gly Glu Glu Ser
                 20                  25                  30

 Thr Gly Thr Asn Ile Gly Glu Ala Leu Gly His Gly Leu Gly Asp
                 35                  40                  45

 Ala Leu Ser Glu Gly Val Gly Lys Ala Ile Gly Lys Glu Ala Gly
```

```
                50                      55                      60
Gly Ala Ala Gly Ser Lys Val Ser Glu Ala Leu Gly Gln Gly Thr
                65                      70                      75
Arg Glu Ala Val Gly Thr Gly Val Arg Gln Val Pro Gly Phe Gly
                80                      85                      90
Ala Ala Asp Ala Leu Gly Asn Arg Val Gly Glu Ala Ala His Ala
                95                     100                     105
Leu Gly Asn Thr Gly His Glu Ile Gly Arg Gln Ala Glu Asp Val
               110                     115                     120
Ile Arg His Gly Ala Asp Ala Val Arg Gly Ser Trp Gln Gly Val
               125                     130                     135
Pro Gly His Ser Gly Ala Trp Glu Thr Ser Gly Gly His Gly Ile
               140                     145                     150
Phe Gly Ser Gln Gly Gly Leu Gly Gly Gln Gly Gln Gly Asn Pro
               155                     160                     165
Gly Gly Leu Gly Thr Pro Trp Val His Gly Tyr Pro Gly Asn Ser
               170                     175                     180
Ala Gly Ser Phe Gly Met Asn Pro Gln Gly Ala Pro Trp Gly Gln
               185                     190                     195
Gly Gly Asn Gly Gly Pro Pro Asn Phe Gly Thr Asn Thr Gln Gly
               200                     205                     210
Ala Val Ala Gln Pro Gly Tyr Gly Ser Val Arg Ala Ser Asn Gln
               215                     220                     225
Asn Glu Gly Cys Thr Asn Pro Pro Pro Ser Gly Ser Gly Gly Gly
               230                     235                     240
Ser Ser Asn Ser Gly Gly Gly Ser Gly Ser Gln Ser Gly Ser Ser
               245                     250                     255
Gly Ser Gly Ser Asn Gly Asp Asn Asn Gly Ser Ser Ser Gly
               260                     265                     270
Gly Ser Ser Ser Gly Ser Ser Ser Gly Ser Ser Ser Gly Gly Ser
               275                     280                     285
Ser Gly Gly Ser Ser Gly Gly Ser Ser Gly Asn Ser Gly Gly Ser
               290                     295                     300
Arg Gly Asp Ser Gly Ser Glu Ser Ser Trp Gly Ser Ser Thr Gly
               305                     310                     315
Ser Ser Ser Gly Asn His Gly Gly Ser Gly Gly Gly Asn Gly His
               320                     325                     330
Lys Pro Gly Cys Glu Lys Pro Gly Asn Glu Ala Arg Gly Ser Gly
               335                     340                     345
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54

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Glu Ser Gly Ile Gln Gly Phe Arg Gly Gln Gly Val Ser Ser Asn
            350             355                 360

Met Arg Glu Ile Ser Lys Glu Gly Asn Arg Leu Leu Gly Gly Ser
            365             370                 375

Gly Asp Asn Tyr Arg Gly Gln Gly Ser Ser Trp Gly Ser Gly Gly
            380             385                 390

Gly Asp Ala Val Gly Gly Val Asn Thr Val Asn Ser Glu Thr Ser
            395             400                 405

Pro Gly Met Phe Asn Phe Asp Thr Phe Trp Lys Asn Phe Lys Ser
            410             415                 420

Lys Leu Gly Phe Ile Asn Trp Asp Ala Ile Asn Lys Asp Gln Arg
            425             430                 435

Ser Ser Arg Ile Pro
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<210> 53
<211> 3580
<212> DNA
<213> Homo sapiens

<400> 53
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ctgggagccc agccttccca gaccagccag gggctgcagg cacagctcgc 550

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tgtgttccca gctgtgccct cacggggccc aggcattggc cctggggcgg 800
```

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accagcctgg ccaacatggc aaaaccccat ctctactaaa aataaaaaaa 2250
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56

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<210> 54
<211> 280
<212> PRT
<213> Homo sapiens

<400> 54

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Met Cys Phe Leu Asn Lys Leu Leu Leu Leu Ala Val Leu Gly Trp
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Leu Phe Gln Ile Pro Thr Val Pro Glu Asp Leu Phe Phe Leu Glu
                20                  25                      30

Glu Gly Pro Ser Tyr Ala Phe Glu Val Asp Thr Val Ala Pro Glu
                35                  40                      45

His Gly Leu Asp Asn Ala Pro Val Val Asp Gln Gln Leu Leu Tyr
                50                  55                      60

Thr Cys Cys Pro Tyr Ile Gly Glu Leu Arg Lys Leu Leu Ala Ser
                65                  70                      75

Trp Val Ser Gly Ser Ser Gly Arg Ser Gly Gly Phe Met Arg Lys
                80                  85                      90

Ile Thr Pro Thr Thr Thr Thr Ser Leu Gly Ala Gln Pro Ser Gln
                95                  100                     105

Thr Ser Gln Gly Leu Gln Ala Gln Leu Ala Gln Ala Phe Phe His
                110                 115                     120

Asn Gln Pro Pro Ser Leu Arg Arg Thr Val Glu Phe Val Ala Glu
                125                 130                     135

Arg Ile Gly Ser Asn Cys Val Lys His Ile Lys Ala Thr Leu Val
                140                 145                     150

Ala Asp Leu Val Arg Gln Ala Glu Ser Leu Leu Gln Glu Gln Leu
                155                 160                     165

Val Thr Gln Gly Glu Glu Gly Gly Asp Pro Ala Gln Leu Leu Glu
                170                 175                     180

Ile Leu Cys Ser Gln Leu Cys Pro His Gly Ala Gln Ala Leu Ala
                185                 190                     195

Leu Gly Arg Glu Phe Cys Gln Arg Lys Ser Pro Gly Ala Val Arg
                200                 205                     210

Ala Leu Leu Pro Glu Glu Thr Pro Ala Ala Val Leu Ser Ser Ala
                215                 220                     225

Glu Asn Ile Ala Val Gly Leu Ala Thr Glu Lys Ala Cys Ala Trp
                230                 235                     240

Leu Ser Ala Asn Ile Thr Ala Leu Ile Arg Arg Glu Val Lys Ala
                245                 250                     255

Ala Val Ser Arg Thr Leu Arg Ala Gln Gly Pro Glu Pro Ala Ala
                260                 265                     270

Arg Gly Glu Arg Arg Gly Cys Ser Arg Ala
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58

<210> 55
<211> 2401
<212> DNA
<213> Homo sapiens

<400> 55
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59

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gaggaggcca gcagctagcc attgcacact ggggtgatgg gtgggggcgg 2300

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<210> 56
<211> 299
<212> PRT
<213> Homo sapiens

<400> 56
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Met Ser Ser Asn Lys Glu Gln Arg Ser Ala Val Phe Val Ile Leu
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Phe Ala Leu Ile Thr Ile Leu Ile Leu Tyr Ser Ser Asn Ser Ala
                20                  25                  30
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60

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Asn Glu Val Phe His Tyr Gly Ser Leu Arg Gly Arg Ser Arg Arg
                35                  40                  45

Pro Val Asn Leu Lys Lys Trp Ser Ile Thr Asp Gly Tyr Val Pro
                50                  55                  60

Ile Leu Gly Asn Lys Thr Leu Pro Ser Arg Cys His Gln Cys Val
                65                  70                  75

Ile Val Ser Ser Ser Ser His Leu Leu Gly Thr Lys Leu Gly Pro
                80                  85                  90

Glu Ile Glu Arg Ala Glu Cys Thr Ile Arg Met Asn Asp Ala Pro
                95                  100                 105

Thr Thr Gly Tyr Ser Ala Asp Val Gly Asn Lys Thr Thr Tyr Arg
                110                 115                 120

Val Val Ala His Ser Ser Val Phe Arg Val Leu Arg Arg Pro Gln
                125                 130                 135

Glu Phe Val Asn Arg Thr Pro Glu Thr Val Phe Ile Phe Trp Gly
                140                 145                 150

Pro Pro Ser Lys Met Gln Lys Pro Gln Gly Ser Leu Val Arg Val
                155                 160                 165

Ile Gln Arg Ala Gly Leu Val Phe Pro Asn Met Glu Ala Tyr Ala
                170                 175                 180

Val Ser Pro Gly Arg Met Arg Gln Phe Asp Asp Leu Phe Arg Gly
                185                 190                 195

Glu Thr Gly Lys Asp Arg Glu Lys Ser His Ser Trp Leu Ser Thr
                200                 205                 210

Gly Trp Phe Thr Met Val Ile Ala Val Glu Leu Cys Asp His Val
                215                 220                 225

His Val Tyr Gly Met Val Pro Pro Asn Tyr Cys Ser Gln Arg Pro
                230                 235                 240

Arg Leu Gln Arg Met Pro Tyr His Tyr Tyr Glu Pro Lys Gly Pro
                245                 250                 255

Asp Glu Cys Val Thr Tyr Ile Gln Asn Glu His Ser Arg Lys Gly
                260                 265                 270

Asn His His Arg Phe Ile Thr Glu Lys Arg Val Phe Ser Ser Trp
                275                 280                 285

Ala Gln Leu Tyr Gly Ile Thr Phe Ser His Pro Ser Trp Thr
                290                 295
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<210> 57
<211> 4277
<212> DNA
<213> Homo sapiens

<400> 57

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gctgtggctg aggaatgctg tgcccctcat ctccagccag cgcctccggc  1450
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62

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63

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aataaatgtt tagtcttccc tgtaaaa 4277
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<210> 58
<211> 1115

64

<212> PRT
<213> Homo sapiens

<400> 58
Met Leu Arg Gly Thr Met Thr Ala Trp Arg Gly Met Arg Pro Glu
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Val Thr Leu Ala Cys Leu Leu Leu Ala Thr Ala Gly Cys Phe Ala
                20   25   30

Asp Leu Asn Glu Val Pro Gln Val Thr Val Gln Pro Ala Ser Thr
                35   40   45

Val Gln Lys Pro Gly Gly Thr Val Ile Leu Gly Cys Val Val Glu
                50   55   60

Pro Pro Arg Met Asn Val Thr Trp Arg Leu Asn Gly Lys Glu Leu
                65   70   75

Asn Gly Ser Asp Asp Ala Leu Gly Val Leu Ile Thr His Gly Thr
                80   85   90

Leu Val Ile Thr Ala Leu Asn Asn His Thr Val Gly Arg Tyr Gln
                95   100   105

Cys Val Ala Arg Met Pro Ala Gly Ala Val Ala Ser Val Pro Ala
                110   115   120

Thr Val Thr Leu Ala Asn Leu Gln Asp Phe Lys Leu Asp Val Gln
                125   130   135

His Val Ile Glu Val Asp Glu Gly Asn Thr Ala Val Ile Ala Cys
                140   145   150

His Leu Pro Glu Ser His Pro Lys Ala Gln Val Arg Tyr Ser Val
                155   160   165

Lys Gln Glu Trp Leu Glu Ala Ser Arg Gly Asn Tyr Leu Ile Met
                170   175   180

Pro Ser Gly Asn Leu Gln Ile Val Asn Ala Ser Gln Glu Asp Glu
                185   190   195

Gly Met Tyr Lys Cys Ala Ala Tyr Asn Pro Val Thr Gln Glu Val
                200   205   210

Lys Thr Ser Gly Ser Ser Asp Arg Leu Arg Val Arg Arg Ser Thr
                215   220   225

Ala Glu Ala Ala Arg Ile Ile Tyr Pro Pro Glu Ala Gln Thr Ile
                230   235   240

Ile Val Thr Lys Gly Gln Ser Leu Ile Leu Glu Cys Val Ala Ser
                245   250   255

Gly Ile Pro Pro Pro Arg Val Thr Trp Ala Lys Asp Gly Ser Ser
                260   265   270

65

Val Thr Gly Tyr Asn Lys Thr Arg Phe Leu Leu Ser Asn Leu Leu
                275   280   285

Ile Asp Thr Thr Ser Glu Glu Asp Ser Gly Thr Tyr Arg Cys Met
                290   295   300

Ala Asp Asn Gly Val Gly Gln Pro Gly Ala Ala Val Ile Leu Tyr
                305   310   315

Asn Val Gln Val Phe Glu Pro Pro Glu Val Thr Met Glu Leu Ser
                320   325   330

Gln Leu Val Ile Pro Trp Gly Gln Ser Ala Lys Leu Thr Cys Glu
                335   340   345

Val Arg Gly Asn Pro Pro Pro Ser Val Leu Trp Leu Arg Asn Ala
                350   355   360

Val Pro Leu Ile Ser Ser Gln Arg Leu Arg Leu Ser Arg Arg Ala
                365   370   375

Leu Arg Val Leu Ser Met Gly Pro Glu Asp Glu Gly Val Tyr Gln
                380   385   390

Cys Met Ala Glu Asn Glu Val Gly Ser Ala His Ala Val Val Gln
                395   400   405

Leu Arg Thr Ser Arg Pro Ser Ile Thr Pro Arg Leu Trp Gln Asp
                410   415   420

Ala Glu Leu Ala Thr Gly Thr Pro Pro Val Ser Pro Ser Lys Leu
                425   430   435

Gly Asn Pro Glu Gln Met Leu Arg Gly Gln Pro Ala Leu Pro Arg
                440   445   450

Pro Pro Thr Ser Val Gly Pro Ala Ser Pro Lys Cys Pro Gly Glu
                455   460   465

Lys Gly Gln Gly Ala Pro Ala Glu Ala Pro Ile Ile Leu Ser Ser
                470   475   480

Pro Arg Thr Ser Lys Thr Asp Ser Tyr Glu Leu Val Trp Arg Pro
                485   490   495

Arg His Glu Gly Ser Gly Arg Ala Pro Ile Leu Tyr Tyr Val Val
                500   505   510

Lys His Arg Lys Gln Val Thr Asn Ser Ser Asp Asp Trp Thr Ile
                515   520   525

Ser Gly Ile Pro Ala Asn Gln His Arg Leu Thr Leu Thr Arg Leu
                530   535   540

Asp Pro Gly Ser Leu Tyr Glu Val Glu Met Ala Ala Tyr Asn Cys
                545   550   555

Ala Gly Glu Gly Gln Thr Ala Met Val Thr Phe Arg Thr Gly Arg

66

```
                    560                   565                   570
Arg Pro Lys Pro Glu Ile Met Ala Ser Lys Glu Gln Gln Ile Gln
                    575                   580                   585
Arg Asp Asp Pro Gly Ala Ser Pro Gln Ser Ser Ser Gln Pro Asp
                    590                   595                   600
His Gly Arg Leu Ser Pro Pro Glu Ala Pro Asp Arg Pro Thr Ile
                    605                   610                   615
Ser Thr Ala Ser Glu Thr Ser Val Tyr Val Thr Trp Ile Pro Arg
                    620                   625                   630
Gly Asn Gly Gly Phe Pro Ile Gln Ser Phe Arg Val Glu Tyr Lys
                    635                   640                   645
Lys Leu Lys Lys Val Gly Asp Trp Ile Leu Ala Thr Ser Ala Ile
                    650                   655                   660
Pro Pro Ser Arg Leu Ser Val Glu Ile Thr Gly Leu Glu Lys Gly
                    665                   670                   675
Thr Ser Tyr Lys Phe Arg Val Arg Ala Leu Asn Met Leu Gly Glu
                    680                   685                   690
Ser Glu Pro Ser Ala Pro Ser Arg Pro Tyr Val Val Ser Gly Tyr
                    695                   700                   705
Ser Gly Arg Val Tyr Glu Arg Pro Val Ala Gly Pro Tyr Ile Thr
                    710                   715                   720
Phe Thr Asp Ala Val Asn Glu Thr Thr Ile Met Leu Lys Trp Met
                    725                   730                   735
Tyr Ile Pro Ala Ser Asn Asn Asn Thr Pro Ile His Gly Phe Tyr
                    740                   745                   750
Ile Tyr Tyr Arg Pro Thr Asp Ser Asp Asn Asp Ser Asp Tyr Lys
                    755                   760                   765
Lys Asp Met Val Glu Gly Asp Lys Tyr Trp His Ser Ile Ser His
                    770                   775                   780'
Leu Gln Pro Glu Thr Ser Tyr Asp Ile Lys Met Gln Cys Phe Asn
                    785                   790                   795
Glu Gly Gly Glu Ser Glu Phe Ser Asn Val Met Ile Cys Glu Thr
                    800                   805                   810
Lys Ala Arg Lys Ser Ser Gly Gln Pro Gly Arg Leu Pro Pro Pro
                    815                   820                   825
Thr Leu Ala Pro Pro Gln Pro Pro Leu Pro Glu Thr Ile Glu Arg
                    830                   835                   840
Pro Val Gly Thr Gly Ala Met Val Ala Arg Ser Ser Asp Leu Pro
                    845                   850                   855
```

67

```
Tyr Leu Ile Val Gly Val Val Leu Gly Ser Ile Val Leu Ile Ile
            860             865             870

Val Thr Phe Ile Pro Phe Cys Leu Trp Arg Ala Trp Ser Lys Gln
            875             880             885

Lys His Thr Thr Asp Leu Gly Phe Pro Arg Ser Ala Leu Pro Pro
            890             895             900

Ser Cys Pro Tyr Thr Met Val Pro Leu Gly Gly Leu Pro Gly His
            905             910             915

Gln Ala Ser Gly Gln Pro Tyr Leu Ser Gly Ile Ser Gly Arg Ala
            920             925             930

Cys Ala Asn Gly Ile His Met Asn Arg Gly Cys Pro Ser Ala Ala
            935             940             945

Val Gly Tyr Pro Gly Met Lys Pro Gln Gln His Cys Pro Gly Glu
            950             955             960

Leu Gln Gln Gln Ser Asp Thr Ser Ser Leu Leu Arg Gln Thr His
            965             970             975

Leu Gly Asn Gly Tyr Asp Pro Gln Ser His Gln Ile Thr Arg Gly
            980             985             990

Pro Lys Ser Ser Pro Asp Glu Gly Ser Phe Leu Tyr Thr Leu Pro
            995             1000            1005

Asp Asp Ser Thr His Gln Leu Leu Gln Pro His His Asp Cys Cys
            1010            1015            1020

Gln Arg Gln Glu Gln Pro Ala Ala Val Gly Gln Ser Gly Val Arg
            1025            1030            1035

Arg Ala Pro Asp Ser Pro Val Leu Glu Ala Val Trp Asp Pro Pro
            1040            1045            1050

Phe His Ser Gly Pro Pro Cys Cys Leu Gly Leu Val Pro Val Glu
            1055            1060            1065

Glu Val Asp Ser Pro Asp Ser Cys Gln Val Ser Gly Gly Asp Trp
            1070            1075            1080

Cys Pro Gln His Pro Val Gly Ala Tyr Val Gly Gln Glu Pro Gly
            1085            1090            1095

Met Gln Leu Ser Pro Gly Pro Leu Val Arg Val Ser Phe Glu Thr
            1100            1105            1110

Pro Pro Leu Thr Ile
            1115

<210> 59
<211> 25
<212> DNA
<213> Artificial
```

68

<220>
<221> Artificial sequence
<222> 1-25
<223> Synthetic construct.

<400> 59
gggaaacaca gcagtcattg cctgc 25

<210> 60
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-24
<223> Synthetic construct.

<400> 60
gcacacgtag cctgtcgctg gagc 24

<210> 61
<211> 42
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-42
<223> Synthetic construct.

<400> 61
caccccaaag cccaggtccg gtacagcgtc aaacaagagt gg 42

<210> 62
<211> 1661
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 678
<223> unknown base

<400> 62
cgggaggctg ggtcgtcatg atccggaccc cattgtcggc ctctgcccat 50

cgcctgctcc tcccaggctc ccgcggccga cccccgcgca acatgcagcc 100

cacgggccgc gagggttccc gcgcgctcag ccggcggtat ctgcggcgtc 150

tgctgctcct gctactgctg ctgctgctgc ggcagcccgt aacccgcgcg 200

gagaccacgc cgggcgcccc cagagccctc tccacgctgg gctcccccag 250

cctcttcacc acgccgggtg tccccagcgc cctcactacc ccaggcctca 300

ctacgccagg cacccccaaa accctggacc ttcggggtcg cgcgcaggcc 350

69

```
ctgatgcgga gtttcccact cgtggacggc cacaatgacc tgccccaggt 400

cctgagacag cgttacaaga atgtgcttca ggatgttaac ctgcgaaatt 450

tcagccatgg tcagaccagc ctggacaggc ttagagacgg cctcgtgggt 500

gcccagttct ggtcagcctc cgtctcatgc cagtcccagg accagactgc 550

cgtgcgcctc gccctggagc agattgacct cattcaccgc atgtgtgcct 600

cctactctga actcgagctt gtgacctcag ctgaaggtct gaacagctct 650

caaaagctgg cctgcctcat tggcgtgnag ggtggtcact cactggacag 700

cagcctctct gtgctgcgca gtttctatgt gctggggggtg cgctacctga 750

cacttacctt cacctgcagt acaccatggg cagagagttc caccaagttc 800

agacaccaca tgtacaccaa cgtcagcgga ttgacaagct ttggtgagaa 850

agtagtagag gagttgaacc gcctgggcat gatgatagat ttgtcctatg 900

catcggacac cttgataaga agggtcctgg aagtgtctca ggctcctgtg 950

atcttctccc actcagctgc cagagctgtg tgtgacaatt tgttgaatgt 1000

tcccgatgat atcctgcagc ttctgaagaa cggtggcatc gtgatggtga 1050

cactgtccat gggggtgctg cagtgcaacc tgcttgctaa cgtgtccact 1100

gtggcagatc actttgacca catcagggca gtcattggat ctgagttcat 1150

cgggattggt ggaaattatg acgggactgg ccggttccct cagggctgg 1200

aggatgtgtc cacataccca gtcctgatag aggagttgct gagtcgtasc 1250

tggagcgagg aagagcttca aggtgtcctt cgtggaaacc tgctgcgggt 1300

cttcagacaa gtggaaaagg tgagagagga gagcagggcg cagagccccg 1350

tggaggctga gtttccatat gggcaactga gcacatcctg ccactcccac 1400

ctcgtgcctc agaatggaca ccaggctact catctggagg tgaccaagca 1450

gccaaccaat cgggtcccct ggaggtcctc aaatgcctcc ccataccttg 1500

ttccaggcct tgtggctgct gccaccatcc caaccttcac ccagtggctc 1550

tgctgacaca gtcggtcccc gcagaggtca ctgtggcaaa gcctcacaaa 1600

gcccctctc ctagttcatt cacaagcata tgctgagaat aaacatgtta 1650

cacatggaaa a 1661
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<210> 63
<211> 487
<212> PRT
<213> Homo sapiens

70

<220>
<221> unsure
<222> 196, 386
<223> unknown amino acid

<400> 63
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Met Gln Pro Thr Gly Arg Glu Gly Ser Arg Ala Leu Ser Arg Arg
 1               5                  10                      15

Tyr Leu Arg Arg Leu Leu Leu Leu Leu Leu Leu Leu Leu Leu Arg
                  20                  25                  30

Gln Pro Val Thr Arg Ala Glu Thr Thr Pro Gly Ala Pro Arg Ala
                  35                  40                  45

Leu Ser Thr Leu Gly Ser Pro Ser Leu Phe Thr Thr Pro Gly Val
                  50                  55                  60

Pro Ser Ala Leu Thr Thr Pro Gly Leu Thr Thr Pro Gly Thr Pro
                  65                  70                  75

Lys Thr Leu Asp Leu Arg Gly Arg Ala Gln Ala Leu Met Arg Ser
                  80                  85                  90

Phe Pro Leu Val Asp Gly His Asn Asp Leu Pro Gln Val Leu Arg
                  95                 100                 105

Gln Arg Tyr Lys Asn Val Leu Gln Asp Val Asn Leu Arg Asn Phe
                 110                 115                 120

Ser His Gly Gln Thr Ser Leu Asp Arg Leu Arg Asp Gly Leu Val
                 125                 130                 135

Gly Ala Gln Phe Trp Ser Ala Ser Val Ser Cys Gln Ser Gln Asp
                 140                 145                 150

Gln Thr Ala Val Arg Leu Ala Leu Glu Gln Ile Asp Leu Ile His
                 155                 160                 165

Arg Met Cys Ala Ser Tyr Ser Glu Leu Glu Leu Val Thr Ser Ala
                 170                 175                 180

Glu Gly Leu Asn Ser Ser Gln Lys Leu Ala Cys Leu Ile Gly Val
                 185                 190                 195

Xaa Gly Gly His Ser Leu Asp Ser Ser Leu Ser Val Leu Arg Ser
                 200                 205                 210

Phe Tyr Val Leu Gly Val Arg Tyr Leu Thr Leu Thr Phe Thr Cys
                 215                 220                 225

Ser Thr Pro Trp Ala Glu Ser Ser Thr Lys Phe Arg His His Met
                 230                 235                 240

Tyr Thr Asn Val Ser Gly Leu Thr Ser Phe Gly Glu Lys Val Val
                 245                 250                 255

Glu Glu Leu Asn Arg Leu Gly Met Met Ile Asp Leu Ser Tyr Ala
```

71

Ser Asp Thr Leu Ile Arg Arg Val Leu Glu Val Ser Gln Ala Pro
            275   280   285

Val Ile Phe Ser His Ser Ala Ala Arg Ala Val Cys Asp Asn Leu
            290   295   300

Leu Asn Val Pro Asp Asp Ile Leu Gln Leu Leu Lys Asn Gly Gly
            305   310   315

Ile Val Met Val Thr Leu Ser Met Gly Val Leu Gln Cys Asn Leu
            320   325   330

Leu Ala Asn Val Ser Thr Val Ala Asp His Phe Asp His Ile Arg
            335   340   345

Ala Val Ile Gly Ser Glu Phe Ile Gly Ile Gly Gly Asn Tyr Asp
            350   355   360

Gly Thr Gly Arg Phe Pro Gln Gly Leu Glu Asp Val Ser Thr Tyr
            365   370   375

Pro Val Leu Ile Glu Glu Leu Leu Ser Arg Xaa Trp Ser Glu Glu
            380   385   390

Glu Leu Gln Gly Val Leu Arg Gly Asn Leu Leu Arg Val Phe Arg
            395   400   405

Gln Val Glu Lys Val Arg Glu Glu Ser Arg Ala Gln Ser Pro Val
            410   415   420

Glu Ala Glu Phe Pro Tyr Gly Gln Leu Ser Thr Ser Cys His Ser
            425   430   435

His Leu Val Pro Gln Asn Gly His Gln Ala Thr His Leu Glu Val
            440   445   450

Thr Lys Gln Pro Thr Asn Arg Val Pro Trp Arg Ser Ser Asn Ala
            455   460   465

Ser Pro Tyr Leu Val Pro Gly Leu Val Ala Ala Ala Thr Ile Pro
            470   475   480

Thr Phe Thr Gln Trp Leu Cys
            485

<210> 64
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-25
<223> Synthetic construct.

<400> 64

ccttcacctg cagtacacca tgggc 25

<210> 65
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-25
<223> Synthetic construct.

<400> 65
 gtcacacaca gctctggcag ctgag 25

<210> 66
<211> 47
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-47
<223> Synthetic construct.

<400> 66
 ccaagttcag acaccacatg tacaccaacg tcagcggatt gacaagc 47

<210> 67
<211> 1564
<212> DNA
<213> Homo sapiens

<400> 67
 tgctaggctc tgtcccacaa tgcacccgag agcaggagct gaaagcctct 50

 aacacccaca gatccctcta tgactgcaat gtgaggtgtc cggctttgct 100

 ggcccagcaa gcctgataag catgaagctc ttatctttgg tggctgtggt 150

 cgggtgtttg ctggtgcccc cagctgaagc caacaagagt tctgaagata 200

 tccggtgcaa atgcatctgt ccaccttata gaaacatcag tgggcacatt 250

 tacaaccaga atgtatccca gaaggactgc aactgcctgc acgtggtgga 300

 gcccatgcca gtgcctggcc atgacgtgga ggcctactgc ctgctgtgcg 350

 agtgcaggta cgaggagcgc agcaccacca ccatcaaggt catcattgtc 400

 atctacctgt ccgtggtggg tgccctgttg ctctacatgg ccttcctgat 450

 gctggtggac cctctgatcc gaaagccgga tgcatacact gagcaactgc 500

 acaatgagga ggagaatgag gatgctcgct ctatggcagc agctgctgca 550

 tccctcgggg gaccccgagc aaacacagtc ctggagcgtg tggaaggtgc 600

73

```
ccagcagcgg tggaagctgc aggtgcagga gcagcggaag acagtcttcg 650

atcggcacaa gatgctcagc tagatgggct ggtgtggttg ggtcaaggcc 700

ccaacaccat ggctgccagc ttccaggctg acaaagcag ggggctactt 750

ctcccttccc tcggttccag tcttcccttt aaaagcctgt ggcatttttc 800

ctccttctcc ctaactttag aaatgttgta cttggctatt ttgattaggg 850

aagagggatg tggtctctga tctctgttgt cttcttgggt ctttgggggtt 900

gaagggaggg ggaaggcagg ccagaaggga atggagacat tcgaggcggc 950

ctcaggagtg gatgcgatct gtctctcctg gctccactct tgccgccttc 1000

cagctctgag tcttgggaat gttgttaccc ttggaagata aagctgggtc 1050

ttcaggaact cagtgtctgg gaggaaagca tggcccagca ttcagcatgt 1100

gttcctttct gcagtggttc ttatcaccac ctccctccca gccccggcgc 1150

ctcagcccca gccccagctc cagccctgag gacagctctg atgggagagc 1200

tgggcccct gagcccactg ggtcttcagg gtgcactgga agctggtgtt 1250

cgctgtcccc tgtgcacttc tcgcactggg gcatggagtg cccatgcata 1300

ctctgctgcc ggtcccctca cctgcacttg aggggtctgg gcagtccctc 1350

ctctccccag tgtccacagt cactgagcca gacggtcggt tggaacatga 1400

gactcgaggc tgagcgtgga tctgaacacc acagccctg tacttgggtt 1450

gcctcttgtc cctgaacttc gttgtaccag tgcatggaga gaaaattttg 1500

tcctcttgtc ttagagttgt gtgtaaatca aggaagccat cattaaattg 1550

ttttatttct ctca 1564
```

<210> 68
<211> 183
<212> PRT
<213> Homo sapiens

<400> 68

```
Met Lys Leu Leu Ser Leu Val Ala Val Val Gly Cys Leu Leu Val
 1               5                  10                  15

Pro Pro Ala Glu Ala Asn Lys Ser Ser Glu Asp Ile Arg Cys Lys
                20              25                  30

Cys Ile Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn
                35              40                  45

Gln Asn Val Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu
                50              55                  60
```

74

```
Pro Met Pro Val Pro Gly His Asp Val Glu Ala Tyr Cys Leu Leu
                65                  70                  75

Cys Glu Cys Arg Tyr Glu Glu Arg Ser Thr Thr Thr Ile Lys Val
                80                  85                  90

Ile Ile Val Ile Tyr Leu Ser Val Val Gly Ala Leu Leu Leu Tyr
                95                 100                 105

Met Ala Phe Leu Met Leu Val Asp Pro Leu Ile Arg Lys Pro Asp
               110                 115                 120

Ala Tyr Thr Glu Gln Leu His Asn Glu Glu Glu Asn Glu Asp Ala
               125                 130                 135

Arg Ser Met Ala Ala Ala Ala Ala Ser Leu Gly Gly Pro Arg Ala
               140                 145                 150

Asn Thr Val Leu Glu Arg Val Glu Gly Ala Gln Gln Arg Trp Lys
               155                 160                 165

Leu Gln Val Gln Glu Gln Arg Lys Thr Val Phe Asp Arg His Lys
               170                 175                 180

Met Leu Ser


<210> 69
<211> 3170
<212> DNA
<213> Homo sapiens

<400> 69
agcgggtctc gcttgggttc cgctaatttc tgtcctgagg cgtgagactg 50

agttcatagg gtcctgggtc cccgaaccag gaagggttga gggaacacaa 100

tctgcaagcc cccgcgaccc aagtgagggg ccccgtgttg gggtcctccc 150

tccctttgca ttcccacccc tccgggcttt gcgtcttcct ggggaccccc 200

tcgccgggag atggccgcgt tgatgcggag caaggattcg tcctgctgcc 250

tgctcctact ggccgcggtg ctgatggtgg agagctcaca gatcggcagt 300

tcgcgggcca aactcaactc catcaagtcc tctctgggcg gggagacgcc 350

tggtcaggcc gccaatcgat ctgcgggcat gtaccaagga ctggcattcg 400

gcggcagtaa gaagggcaaa aacctggggc aggcctaccc ttgtagcagt 450

gataaggagt gtgaagttgg gaggtattgc acagtcccc accaaggatc 500

atcggcctgc atggtgtgtc ggagaaaaaa gaagcgctgc caccgagatg 550

gcatgtgctg ccccagtacc cgctgcaata atggcatctg tatcccagtt 600

actgaaagca tcttaacccc tcacatcccg gctctggatg gtactcggca 650
```

```
cagagatcga aaccacggtc attactcaaa ccatgacttg ggatggcaga 700

atctaggaag accacacact aagatgtcac atataaaagg gcatgaagga 750

gaccccctgcc tacgatcatc agactgcatt gaagggtttt gctgtgctcg 800

tcatttctgg accaaaatct gcaaaccagt gctccatcag ggggaagtct 850

gtaccaaaca acgcaagaag ggttctcatg ggctggaaat tttccagcgt 900

tgcgactgtg cgaagggcct gtcttgcaaa gtatggaaag atgccaccta 950

ctcctccaaa gccagactcc atgtgtgtca gaaaatttga tcaccattga 1000

ggaacatcat caattgcaga ctgtgaagtt gtgtatttaa tgcattatag 1050

catggtggaa aataaggttc agatgcagaa gaatggctaa aataagaaac 1100

gtgataagaa tatagatgat cacaaaaagg gagaaagaaa acatgaactg 1150

aatagattag aatgggtgac aaatgcagtg cagccagtgt ttccattatg 1200

caacttgtct atgtaaataa tgtacacatt tgtggaaaat gctattatta 1250

agagaacaag cacacagtgg aaattactga tgagtagcat gtgactttcc 1300

aagagtttag gttgtgctgg aggagaggtt tccttcagat tgctgattgc 1350

ttatacaaat aacctacatg ccagatttct attcaacgtt agagtttaac 1400

aaaatactcc tagaataact tgttatacaa taggttctaa aaataaaatt 1450

gctaaacaag aaatgaaaac atggagcatt gttaatttac aacagaaaat 1500

tacctttttga tttgtaacac tacttctgct gttcaatcaa gagtcttggt 1550

agataagaaa aaaatcagtc aatatttcca ataattgca aaataatggc 1600

cagttgttta ggaaggcctt taggaagaca aataaataac aaacaaacag 1650

ccacaaatac ttttttttca aaattttagt tttacctgta attaataaga 1700

actgatacaa gacaaaaaca gttccttcag attctacgga atgacagtat 1750

atctctcttt atcctatgtg attcctgctc tgaatgcatt atattttcca 1800

aactataccc ataaattgtg actagtaaaa tacttacaca gagcagaatt 1850

ttcacagatg gcaaaaaaat ttaaagatgt ccaatatatg tgggaaaaga 1900

gctaacagag agatcattat ttcttaaaga ttggccataa cctatatttt 1950

gatagaatta gattggtaaa tacatgtatt catacatact ctgtggtaat 2000

agagacttaa gctggatctg tactgcactg gagtaagcaa gaaaattggg 2050

aaaactttttt cgtttgttca ggttttggca acacatagat catatgtctg 2100
```

76

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aggcacaagt tggctgttca tctttgaaac caggggatgc acagtctaaa 2150

tgaatatctg catgggattt gctatcataa tatttactat gcagatgaat 2200

tcagtgtgag gtcctgtgtc cgtactatcc tcaaattatt tattttatag 2250

tgctgagatc ctcaaataat ctcaatttca ggaggtttca caaaatgtac 2300

tcctgaagta gacagagtag tgaggtttca ttgccctcta taagcttctg 2350

actagccaat ggcatcatcc aattttcttc ccaaacctct gcagcatctg 2400

ctttattgcc aaagggctag tttcggtttt ctgcagccat tgcggttaaa 2450

aaatataagt aggataactt gtaaaacctg catattgcta atctatagac 2500

accacagttt ctaaattctt tgaaaccact ttactacttt ttttaaactt 2550

aactcagttc taaatacttt gtctggagca caaaacaata aaaggttatc 2600

ttatagtcgt gactttaaac ttttgtagac cacaattcac tttttagttt 2650

tcttttactt aaatcccatc tgcagtctca aatttaagtt ctcccagtag 2700

agattgagtt tgagcctgta tatctattaa aaatttcaac ttcccacata 2750

tatttactaa gatgattaag acttacattt tctgcacagg tctgcaaaaa 2800

caaaaattat aaactagtcc atccaagaac caaagtttgt ataaacaggt 2850

tgctataagc ttgtgaaatg aaaatggaac atttcaatca aacatttcct 2900

atataacaat tattatattt acaatttggt ttctgcaata tttttcttat 2950

gtccaccctt ttaaaaatta ttatttgaag taattatttt acaggaaatg 3000

ttaatgagat gtattttctt atagagatat ttcttacaga aagctttgta 3050

gcagaatata tttgcagcta ttgactttgt aatttaggaa aaatgtataa 3100

taagataaaa tctattaaat ttttctcctc taaaaactga aaaaaaaaaa 3150

aaaaaaaaaa aaaaaaaaaa 3170
```

<210> 70
<211> 259
<212> PRT
<213> Homo sapiens

<400> 70
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Met Ala Ala Leu Met Arg Ser Lys Asp Ser Ser Cys Cys Leu Leu
 1               5                  10                  15

Leu Leu Ala Ala Val Leu Met Val Glu Ser Ser Gln Ile Gly Ser
                20                  25                  30

Ser Arg Ala Lys Leu Asn Ser Ile Lys Ser Ser Leu Gly Gly Glu
                35                  40                  45
```

```
Thr Pro Gly Gln Ala Ala Asn Arg Ser Ala Gly Met Tyr Gln Gly
                50              55                      60

Leu Ala Phe Gly Gly Ser Lys Lys Gly Lys Asn Leu Gly Gln Ala
                65              70                      75

Tyr Pro Cys Ser Ser Asp Lys Glu Cys Glu Val Gly Arg Tyr Cys
                80              85                      90

His Ser Pro His Gln Gly Ser Ser Ala Cys Met Val Cys Arg Arg
                95              100                     105

Lys Lys Lys Arg Cys His Arg Asp Gly Met Cys Cys Pro Ser Thr
                110             115                     120

Arg Cys Asn Asn Gly Ile Cys Ile Pro Val Thr Glu Ser Ile Leu
                125             130                     135

Thr Pro His Ile Pro Ala Leu Asp Gly Thr Arg His Arg Asp Arg
                140             145                     150

Asn His Gly His Tyr Ser Asn His Asp Leu Gly Trp Gln Asn Leu
                155             160                     165

Gly Arg Pro His Thr Lys Met Ser His Ile Lys Gly His Glu Gly
                170             175                     180

Asp Pro Cys Leu Arg Ser Ser Asp Cys Ile Glu Gly Phe Cys Cys
                185             190                     195

Ala Arg His Phe Trp Thr Lys Ile Cys Lys Pro Val Leu His Gln
                200             205                     210

Gly Glu Val Cys Thr Lys Gln Arg Lys Lys Gly Ser His Gly Leu
                215             220                     225

Glu Ile Phe Gln Arg Cys Asp Cys Ala Lys Gly Leu Ser Cys Lys
                230             235                     240

Val Trp Lys Asp Ala Thr Tyr Ser Ser Lys Ala Arg Leu His Val
                245             250                     255

Cys Gln Lys Ile

<210> 71
<211> 1809
<212> DNA
<213> Homo sapiens

<400> 71
 tctcaatctg ctgacctcgt gatccgcctg accttgtaat ccacctacct 50

 tggcctccca aagtgttggg attacaggcg tgagccaccg cgcccggcca 100

 acatcacgtt tttaaaaatt gatttcttca aattcatggc aaatatttcc 150

 cttccctttg acttcttatg tcagaatgag gaaggatagc tgcatttatt 200
```
78

```
tagtcagttt  tcattgcata  gtaatatttt  catgtagtat  tttctaagtt  250

atattttagt  aattcatatg  ttttagatta  taggtttttaa  catacttgtg  300

aaaatacttg  atgtgtttta  aagccttggg  cagaaattct  gtattgttga  350

ggatttgttc  ttttatcccc  cttttaaagt  catccgtcct  tggctcagga  400

tttggagagc  ttgcaccacc  aaaaatggca  aacatcacca  gctcccagat  450

tttggaccag  ttgaaagctc  cgagtttggg  ccagtttacc  accaccccaa  500

gtacacagca  gaatagtaca  agtcaccta  caactactac  ttcttgggac  550

ctcaagcccc  caacatccca  gtcctcagtc  ctcagtcatc  ttgacttcaa  600

atctcaacct  gagccatccc  cagttcttag  ccagttgagc  cagcgacaac  650

agcaccagag  ccaggcagtc  actgttcctc  ctcctggttt  ggagtccttt  700

ccttcccagg  caaaacttcg  agaatcaaca  cctggagaca  gtccctccac  750

tgtgaacaag  cttttgcagc  ttcccagcac  gaccattgaa  aatatctctg  800

tgtctgtcca  ccagccacag  cccaaacaca  tcaaacttgc  taagcggcgg  850

ataccccag  cttctaagat  cccagcttct  gcagtggaaa  tgcctggttc  900

agcagatgtc  acaggattaa  atgtgcagtt  tggggctctg  gaatttgggt  950

cagaaccttc  tctctctgaa  tttggatcag  ctccaagcag  tgaaaatagt  1000

aatcagattc  ccatcagctt  gtattcgaag  tctttaagtg  agcctttgaa  1050

tacatcttta  tcaatgacca  gtgcagtaca  gaactccaca  tatacaactt  1100

ccgtcattac  ctcctgcagt  ctgacaagct  catcactgaa  ttctgctagt  1150

ccagtagcaa  tgtcttcctc  ttatgaccag  agttctgtgc  ataacaggat  1200

cccataccaa  agccctgtga  gttcatcaga  gtcagctcca  ggaaccatca  1250

tgaatggaca  tggtggtggt  cgaagtcagc  agacactaga  cagtaagtat  1300

agcagcaagc  tactcttgtc  atggctggtg  ccaaccaaac  agaggaagag  1350

gatagctcac  gtgatgtgga  aaacaccagt  tggtcaatgg  ctcattcgtt  1400

aaaaagcagc  cctttgctt  ttttgttttt  ggaccaggtg  ttggctgtgg  1450

tgttattaga  aatgtcttaa  ccacagcaag  aaggaggtgg  tggtctcata  1500

ttcttctgcc  ctaatcagac  tgcaccacaa  gtgcagcata  cagtatgcat  1550

tttaaagatg  cttgggccag  gcggggtggc  tgatgcccat  aatcccagtg  1600

ctttgggggg  ccaaggcagg  cagattgccc  aagctcagga  gtttgagacc  1650
```

79

accctgggca acatggtgaa actctgtctc tactaaaata cgaaaaacta 1700

gccgggtgtg gtggcggcgc gtgcctgtaa tcccagctac ttgggaggct 1750

gaggcacaag aatcgcttga gccagcttgg gctacaaagt gagactccgt 1800

ctgaaaaga 1809

<210> 72
<211> 363
<212> PRT
<213> Homo sapiens

<400> 72
```
Met Cys Phe Lys Ala Leu Gly Arg Asn Ser Val Leu Leu Arg Ile
 1               5                  10                  15

Cys Ser Phe Ile Pro Leu Leu Lys Ser Ser Val Leu Gly Ser Gly
                20                  25                  30

Phe Gly Glu Leu Ala Pro Pro Lys Met Ala Asn Ile Thr Ser Ser
                35                  40                  45

Gln Ile Leu Asp Gln Leu Lys Ala Pro Ser Leu Gly Gln Phe Thr
                50                  55                  60

Thr Thr Pro Ser Thr Gln Gln Asn Ser Thr Ser His Pro Thr Thr
                65                  70                  75

Thr Thr Ser Trp Asp Leu Lys Pro Pro Thr Ser Gln Ser Ser Val
                80                  85                  90

Leu Ser His Leu Asp Phe Lys Ser Gln Pro Glu Pro Ser Pro Val
                95                  100                 105

Leu Ser Gln Leu Ser Gln Arg Gln Gln His Gln Ser Gln Ala Val
                110                 115                 120

Thr Val Pro Pro Pro Gly Leu Glu Ser Phe Pro Ser Gln Ala Lys
                125                 130                 135

Leu Arg Glu Ser Thr Pro Gly Asp Ser Pro Ser Thr Val Asn Lys
                140                 145                 150

Leu Leu Gln Leu Pro Ser Thr Thr Ile Glu Asn Ile Ser Val Ser
                155                 160                 165

Val His Gln Pro Gln Pro Lys His Ile Lys Leu Ala Lys Arg Arg
                170                 175                 180

Ile Pro Pro Ala Ser Lys Ile Pro Ala Ser Ala Val Glu Met Pro
                185                 190                 195

Gly Ser Ala Asp Val Thr Gly Leu Asn Val Gln Phe Gly Ala Leu
                200                 205                 210

Glu Phe Gly Ser Glu Pro Ser Leu Ser Glu Phe Gly Ser Ala Pro
                215                 220                 225
```

80

```
Ser Ser Glu Asn Ser Asn Gln Ile Pro Ile Ser Leu Tyr Ser Lys
            230             235             240

Ser Leu Ser Glu Pro Leu Asn Thr Ser Leu Ser Met Thr Ser Ala
            245             250             255

Val Gln Asn Ser Thr Tyr Thr Thr Ser Val Ile Thr Ser Cys Ser
            260             265             270

Leu Thr Ser Ser Ser Leu Asn Ser Ala Ser Pro Val Ala Met Ser
            275             280             285

Ser Ser Tyr Asp Gln Ser Ser Val His Asn Arg Ile Pro Tyr Gln
            290             295             300

Ser Pro Val Ser Ser Ser Glu Ser Ala Pro Gly Thr Ile Met Asn
            305             310             315

Gly His Gly Gly Gly Arg Ser Gln Gln Thr Leu Asp Ser Lys Tyr
            320             325             330

Ser Ser Lys Leu Leu Leu Ser Trp Leu Val Pro Thr Lys Gln Arg
            335             340             345

Lys Arg Ile Ala His Val Met Trp Lys Thr Pro Val Gly Gln Trp
            350             355             360

Leu Ile Arg


<210> 73
<211> 26
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-26
<223> Synthetic construct.

<400> 73
 aattcatggc aaatatttcc cttccc 26

<210> 74
<211> 22
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-22
<223> Synthetic construct.

<400> 74
 tggtaaactg gcccaaactc gg 22

<210> 75
<211> 50
```

81

<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-50
<223> Synthetic construct

<400> 75
 ttaaagtcat ccgtccttgg ctcaggattt ggagagcttg caccaccaaa 50

<210> 76
<211> 1989
<212> DNA
<213> Homo sapiens

<400> 76
 gccgagtggg acaaagcctg gggctgggcg ggggccatgg cgctgccatc 50

 ccgaatcctg ctttggaaac ttgtgcttct gcagagctct gctgttctcc 100

 tgcactcagc ggtggaggag acggacgcgg ggctgtacac ctgcaacctg 150

 caccatcact actgccacct ctacgagagc ctggccgtcc gcctggaggt 200

 caccgacggc cccccggcca cccccgccta ctgggacggc gagaaggagg 250

 tgctggcggt ggcgcgcggc gcacccgcgc ttctgacctg cgtgaaccgc 300

 gggcacgtgt ggaccgaccg gcacgtggag gaggctcaac aggtggtgca 350

 ctgggaccgg cagccgcccg gggtcccgca cgaccgcgcg gaccgcctgc 400

 tggacctcta cgcgtcgggc gagcgccgcg cctacgggcc ccttttctg 450

 cgcgaccgcg tggctgtggg cgcggatgcc tttgagcgcg gtgacttctc 500

 actgcgtatc gagccgctgg aggtcgccga cgagggcacc tactcctgcc 550

 acctgcacca ccattactgt ggcctgcacg aacgccgcgt cttccacctg 600

 acggtcgccg aacccacgc ggagccgccc ccccgggggct ctccgggcaa 650

 cggctccagc cacagcggcg ccccaggccc agaccccaca ctggcgcgcg 700

 gccacaacgt catcaatgtc atcgtccccg agagccgagc ccacttcttc 750

 cagcagctgg gctacgtgct ggccacgctg ctgctcttca tcctgctact 800

 ggtcactgtc ctcctggccg cccgcaggcg ccgcggaggc tacgaatact 850

 cggaccagaa gtcgggaaag tcaaagggga aggatgttaa cttggcggag 900

 ttcgctgtgg ctgcagggga ccagatgctt tacaggagtg aggacatcca 950

 gctagattac aaaaacaaca tcctgaagga gagggcggag ctggcccaca 1000

 gcccccctgcc tgccaagtac atcgacctag acaaagggtt ccggaaggag 1050

                              82

```
aactgcaaat agggaggccc tgggctcctg gctgggccag cagctgcacc 1100

tctcctgtct gtgctcctcg gggcatctcc tgatgctccg gggctcaccc 1150

cccttccagc ggctggtccc gctttcctgg aatttggcct gggcgtatgc 1200

agaggccgcc tccacacccc tcccccaggg gcttggtggc agcatagccc 1250

ccacccctgc ggcctttgct cacgggtggc cctgcccacc cctggcacaa 1300

ccaaaatccc actgatgccc atcatgccct cagacccttc tgggctctgc 1350

ccgctggggg cctgaagaca ttcctggagg acactcccat cagaacctgg 1400

cagccccaaa actggggtca gcctcagggc aggagtccca ctcctccagg 1450

gctctgctcg tccggggctg ggagatgttc ctggaggagg acactcccat 1500

cagaacttgg cagccttgaa gttggggtca gcctcggcag gagtcccact 1550

cctcctgggg tgctgcctgc caccaagagc tcccccacct gtaccaccat 1600

gtgggactcc aggcaccatc tgttctcccc agggacctgc tgacttgaat 1650

gccagccctt gctcctctgt gttgctttgg gccacctggg gctgcacccc 1700

ctgccctttc tctgccccat ccctaccta gccttgctct cagccacctt 1750

gatagtcact gggctccctg tgacttctga ccctgacacc cctcccttgg 1800

actctgcctg ggctggagtc tagggctggg gctacatttg gcttctgtac 1850

tggctgagga caggggaggg agtgaagttg gtttggggtg gcctgtgttg 1900

ccactctcag caccccacat ttgcatctgc tggtggacct gccaccatca 1950

caataaagtc cccatctgat ttttaaaaaa aaaaaaaaa 1989
```

<210> 77
<211> 341
<212> PRT
<213> Homo sapiens

<400> 77

```
Met Ala Leu Pro Ser Arg Ile Leu Leu Trp Lys Leu Val Leu Leu
 1               5                  10                  15

Gln Ser Ser Ala Val Leu Leu His Ser Ala Val Glu Glu Thr Asp
                20                  25                  30

Ala Gly Leu Tyr Thr Cys Asn Leu His His Tyr Cys His Leu
                35                  40                  45

Tyr Glu Ser Leu Ala Val Arg Leu Glu Val Thr Asp Gly Pro Pro
                50                  55                  60

Ala Thr Pro Ala Tyr Trp Asp Gly Glu Lys Glu Val Leu Ala Val
                65                  70                  75
```

```
Ala Arg Gly Ala Pro Ala Leu Leu Thr Cys Val Asn Arg Gly His
                80                      85                      90

Val Trp Thr Asp Arg His Val Glu Glu Ala Gln Gln Val Val His
                95                     100                     105

Trp Asp Arg Gln Pro Pro Gly Val Pro His Asp Arg Ala Asp Arg
               110                     115                     120

Leu Leu Asp Leu Tyr Ala Ser Gly Glu Arg Arg Ala Tyr Gly Pro
               125                     130                     135

Leu Phe Leu Arg Asp Arg Val Ala Val Gly Ala Asp Ala Phe Glu
               140                     145                     150

Arg Gly Asp Phe Ser Leu Arg Ile Glu Pro Leu Glu Val Ala Asp
               155                     160                     165

Glu Gly Thr Tyr Ser Cys His Leu His His Tyr Cys Gly Leu
               170                     175                     180

His Glu Arg Arg Val Phe His Leu Thr Val Ala Glu Pro His Ala
               185                     190                     195

Glu Pro Pro Pro Arg Gly Ser Pro Gly Asn Gly Ser Ser His Ser
               200                     205                     210

Gly Ala Pro Gly Pro Asp Pro Thr Leu Ala Arg Gly His Asn Val
               215                     220                     225

Ile Asn Val Ile Val Pro Glu Ser Arg Ala His Phe Phe Gln Gln
               230                     235                     240

Leu Gly Tyr Val Leu Ala Thr Leu Leu Leu Phe Ile Leu Leu Leu
               245                     250                     255

Val Thr Val Leu Leu Ala Ala Arg Arg Arg Arg Gly Gly Tyr Glu
               260                     265                     270

Tyr Ser Asp Gln Lys Ser Gly Lys Ser Lys Gly Lys Asp Val Asn
               275                     280                     285

Leu Ala Glu Phe Ala Val Ala Ala Gly Asp Gln Met Leu Tyr Arg
               290                     295                     300

Ser Glu Asp Ile Gln Leu Asp Tyr Lys Asn Asn Ile Leu Lys Glu
               305                     310                     315

Arg Ala Glu Leu Ala His Ser Pro Leu Pro Ala Lys Tyr Ile Asp
               320                     325                     330

Leu Asp Lys Gly Phe Arg Lys Glu Asn Cys Lys
               335                     340
```

<210> 78
<211> 2243
<212> DNA
<213> Homo sapiens

84

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cgccggaggc agcggcggcg tggcgcagcg gcgacatggc cgttgtctca 50

gaggacgact ttcagcacag ttcaaactcc acctacggaa ccacaagcag 100

cagtctccga gctgaccagg aggcactgct tgagaagctg ctggaccgcc 150

cgcccctgg cctgcagagg cccgaggacc gcttctgtgg cacatacatc 200

atcttcttca gcctgggcat tggcagtcta ctgccatgga acttctttat 250

cactgccaag gagtactgga tgttcaaact ccgcaactcc tccagcccag 300

ccaccgggga ggaccctgag ggctcagaca tcctgaacta ctttgagagc 350

taccttgccg ttgcctccac cgtgccctcc atgctgtgcc tggtggccaa 400

cttcctgctt gtcaacaggg ttgcagtcca catccgtgtc ctggcctcac 450

tgacggtcat cctggccatc ttcatggtga taactgcact ggtgaaggtg 500

gacacttcct cctggacccg tggttttttt gcggtcacca ttgtctgcat 550

ggtgatcctc agcggtgcct ccactgtctt cagcagcagc atctacggca 600

tgaccggctc ctttcctatg aggaactccc aagcactgat atcaggagga 650

gccatgggcg ggacggtcag cgccgtggcc tcattggtgg acttggctgc 700

atccagtgat gtgaggaaca cgcccctggc cttcttcctg acggccacca 750

tcttcctcgt gctctgcatg ggactctacc tgctgctgtc caggctggag 800

tatgccaggt actacatgag gcctgttctt cgggcccatg tgttttctgg 850

tgaagaggag cttccccagg actccctcag tgccccttcg gtggcctcca 900

gattcattga ttcccacaca ccccctctcc gccccatcct gaagaagacg 950

gccagcctgg gcttctgtgt cacctacgtc ttcttcatca ccagcctcat 1000

ctaccccgcc gtctgcacca acatcgagtc cctcaacaag ggctcgggct 1050

cactgtggac caccaagttt ttcatcccccc tcactacctt cctcctgtac 1100

aactttgctg acctatgtgg ccggcagctc accgcctgga tccaggtgcc 1150

agggcccaac agcaaggcgc tcccagggtt cgtgctcctc cggacctgcc 1200

tcatccccct cttcgtgctc tgtaactacc agccccgcgt ccacctgaag 1250

actgtggtct ccagtccga tgtgtacccc gcactcctca gctccctgct 1300

ggggctcagc aacggctacc tcagcaccct ggccctcctc tacgggccta 1350

agattgtgcc cagggagctg gctgaggcca cgggagtggt gatgtccttt 1400

tatgtgtgct tgggcttaac actgggctca gcctgctcta ccctcctggt 1450
```

85

```
gcacctcatc tagaagggag gacacaagga cattggtgct tcagagcctt 1500

tgaagatgag aagagagtgc aggagggctg ggggccatgg aggaaaggcc 1550

taaagtttca cttggggaca gagagcagag cacactcggg cctcatccct 1600

cccaagatgc cagtgagcca cgtccatgcc cattccgtgc aaggcagata 1650

ttccagtcat attaacagaa cactcctgag acagttgaag aagaaatagc 1700

acaaatcagg ggtactccct tcacagctga tggttaacat tccaccttct 1750

ttctagccct tcaaagatgc tgccagtgtt cgccctagag ttattacaaa 1800

gccagtgcca aaacccagcc atgggctctt tgcaacctcc cagctgcgct 1850

cattccagct gacagcgaga tgcaagcaaa tgctcagctc tccttaccct 1900

gaaggggtct ccctggaatg gaagtcccct ggcatggtca gtcctcaggc 1950

ccaagactca agtgtgcaca gacccctgtg ttctgcgggt gaacaactgc 2000

ccactaacca gactggaaaa cccagaaaga tgggccttcc atgaatgctt 2050

cattccagag ggaccagagg gcctccctgt gcaagggatc aagcatgtct 2100

ggcctgggtt ttcaaaaaaa gagggatcct catgacctgg tggtctatgg 2150

cctgggtcaa gatgagggtc tttcagtgtt cctgtttaca acatgtcaaa 2200

gccattggtt caagggcgta ataaatactt gcgtattcaa aaa 2243
```

<210> 79
<211> 475
<212> PRT
<213> Homo sapiens

<400> 79

```
Met Ala Val Val Ser Glu Asp Asp Phe Gln His Ser Ser Asn Ser
 1               5                  10                  15

Thr Tyr Gly Thr Thr Ser Ser Ser Leu Arg Ala Asp Gln Glu Ala
                20                  25                  30

Leu Leu Glu Lys Leu Leu Asp Arg Pro Pro Pro Gly Leu Gln Arg
                35                  40                  45

Pro Glu Asp Arg Phe Cys Gly Thr Tyr Ile Ile Phe Phe Ser Leu
                50                  55                  60

Gly Ile Gly Ser Leu Leu Pro Trp Asn Phe Phe Ile Thr Ala Lys
                65                  70                  75

Glu Tyr Trp Met Phe Lys Leu Arg Asn Ser Ser Ser Pro Ala Thr
                80                  85                  90

Gly Glu Asp Pro Glu Gly Ser Asp Ile Leu Asn Tyr Phe Glu Ser
                95                  100                 105
```

86

```
Tyr Leu Ala Val Ala Ser Thr Val Pro Ser Met Leu Cys Leu Val
            110                 115                 120

Ala Asn Phe Leu Leu Val Asn Arg Val Ala Val His Ile Arg Val
            125                 130                 135

Leu Ala Ser Leu Thr Val Ile Leu Ala Ile Phe Met Val Ile Thr
            140                 145                 150

Ala Leu Val Lys Val Asp Thr Ser Ser Trp Thr Arg Gly Phe Phe
            155                 160                 165

Ala Val Thr Ile Val Cys Met Val Ile Leu Ser Gly Ala Ser Thr
            170                 175                 180

Val Phe Ser Ser Ser Ile Tyr Gly Met Thr Gly Ser Phe Pro Met
            185                 190                 195

Arg Asn Ser Gln Ala Leu Ile Ser Gly Gly Ala Met Gly Gly Thr
            200                 205                 210

Val Ser Ala Val Ala Ser Leu Val Asp Leu Ala Ala Ser Ser Asp
            215                 220                 225

Val Arg Asn Ser Ala Leu Ala Phe Phe Leu Thr Ala Thr Ile Phe
            230                 235                 240

Leu Val Leu Cys Met Gly Leu Tyr Leu Leu Leu Ser Arg Leu Glu
            245                 250                 255

Tyr Ala Arg Tyr Tyr Met Arg Pro Val Leu Ala Ala His Val Phe
            260                 265                 270

Ser Gly Glu Glu Glu Leu Pro Gln Asp Ser Leu Ser Ala Pro Ser
            275                 280                 285

Val Ala Ser Arg Phe Ile Asp Ser His Thr Pro Pro Leu Arg Pro
            290                 295                 300

Ile Leu Lys Lys Thr Ala Ser Leu Gly Phe Cys Val Thr Tyr Val
            305                 310                 315

Phe Phe Ile Thr Ser Leu Ile Tyr Pro Ala Val Cys Thr Asn Ile
            320                 325                 330

Glu Ser Leu Asn Lys Gly Ser Gly Ser Leu Trp Thr Thr Lys Phe
            335                 340                 345

Phe Ile Pro Leu Thr Thr Phe Leu Leu Tyr Asn Phe Ala Asp Leu
            350                 355                 360

Cys Gly Arg Gln Leu Thr Ala Trp Ile Gln Val Pro Gly Pro Asn
            365                 370                 375

Ser Lys Ala Leu Pro Gly Phe Val Leu Leu Arg Thr Cys Leu Ile
            380                 385                 390

Pro Leu Phe Val Leu Cys Asn Tyr Gln Pro Arg Val His Leu Lys
```

87

```
Thr Val Val Phe Gln Ser Asp Val Tyr Pro Ala Leu Leu Ser Ser
                410                    415                    420

Leu Leu Gly Leu Ser Asn Gly Tyr Leu Ser Thr Leu Ala Leu Leu
                425                    430                    435

Tyr Gly Pro Lys Ile Val Pro Arg Glu Leu Ala Glu Ala Thr Gly
                440                    445                    450

Val Val Met Ser Phe Tyr Val Cys Leu Gly Leu Thr Leu Gly Ser
                455                    460                    465

Ala Cys Ser Thr Leu Leu Val His Leu Ile
                470                    475
```

<210> 80
<211> 22
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-22
<223> Synthetic construct.

<400> 80
 ttttgcggtc accattgtct gc 22

<210> 81
<211> 23
<212> DNA
<213> Homo sapiens

<220>
<221> Artificial sequence
<222> 1-23
<223> Synthetic construct.

<400> 81
 cgtaggtgac acagaagccc agg 23

<210> 82
<211> 49
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-49
<223> Synthetic construct.

<400> 82
 tacggcatga ccggctcctt tcctatgagg aactcccagg cactgatat 49

<210> 83
<211> 1844

<212> DNA
<213> Homo sapiens

<400> 83
gacagtggag ggcagtggag aggaccgcgc tgtcctgctg tcaccaagag 50

ctggagacac catctcccac cgagagtcat ggccccattg ccctgcacc 100

tcctcgtcct cgtccccatc ctcctcagcc tggtggcctc ccaggactgg 150

aaggctgaac gcagccaaga ccccttcgag aaatgcatgc aggatcctga 200

ctatgagcag ctgctcaagg tggtgacctg ggggctcaat cggaccctga 250

agccccagag ggtgattgtg gttggcgctg gtgtggccgg gctggtggcc 300

gccaaggtgc tcagcgatgc tggacacaag gtcaccatcc tggaggcaga 350

taacaggatc gggggccgca tcttcaccta ccgggaccag aacacgggct 400

ggattgggga gctgggagcc atgcgcatgc ccagctctca caggatcctc 450

cacaagctct gccagggcct ggggctcaac ctgaccaagt tcacccagta 500

cgacaagaac acgtggacgg aggtgcacga agtgaagctg cgcaactatg 550

tggtggagaa ggtgcccgag aagctgggct acgccttgcg tccccaggaa 600

aagggccact cgcccgaaga catctaccag atggctctca accaggcect 650

caaagacctc aaggcactgg gctgcagaaa ggcgatgaag aagtttgaaa 700

ggcacacgct cttggaatat cttctcgggg aggggaacct gagccggccg 750

gccgtgcagc ttctgggaga cgtgatgtcc gaggatggct tcttctatct 800

cagcttcgcc gaggccctcc gggcccacag ctgcctcagc gacagactcc 850

agtacagccg catcgtgggt ggctgggacc tgctgccgcg cgcgctgctg 900

agctcgctgt ccgggcttgt gctgttgaac gcgcccgtgg tggcgatgac 950

ccagggaccg cacgatgtgc acgtgcagat cgagacctct cccccggcgc 1000

ggaatctgaa ggtgctgaag gccgacgtgg tgctgctgac ggcgagcgga 1050

ccggcggtga agcgcatcac cttctcgccg ccgctgcccc gccacatgca 1100

ggaggcgctg cggaggctgc actacgtgcc ggccaccaag gtgttcctaa 1150

gcttccgcag gcccttctgg cgcgaggagc acattgaagg cggccactca 1200

aacaccgatc gcccgtcgcg catgattttc tacccgccgc cgcgcgaggg 1250

cgcgctgctg ctggcctcgt acacgtggtc ggacgcggcg gcagcgttcg 1300

ccggcttgag ccgggaagag gcgttgcgct tggcgctcga cgacgtggcg 1350

89

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gcattgcacg ggcctgtcgt gcgccagctc tgggacggca ccggcgtcgt 1400

caagcgttgg gcggaggacc agcacagcca gggtggcttt gtggtacagc 1450

cgccggcgct ctggcaaacc gaaaaggatg actggacggt cccttatggc 1500

cgcatctact ttgccggcga gcacaccgcc tacccgcacg gctgggtgga 1550

gacggcggtc aagtcggcgc tgcgcgccgc catcaagatc aacagccgga 1600

agggcctgc atcggacacg gccagccccg aggggcacgc atctgacatg 1650

gaggggcagg ggcatgtgca tggggtggcc agcagccccт cgcatgacct 1700

ggcaaaggaa gaaggcagcc accctccagt ccaaggccag ttatctctcc 1750

aaaacacgac ccacacgagg acctcgcatt aaagtatttt cggaaaaaaa 1800

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1844
```

<210> 84
<211> 567
<212> PRT
<213> Homo sapiens

<400> 84

Met	Ala	Pro	Leu	Ala	Leu	His	Leu	Leu	Val	Leu	Val	Pro	Ile	Leu
1				5					10					15

Leu	Ser	Leu	Val	Ala	Ser	Gln	Asp	Trp	Lys	Ala	Glu	Arg	Ser	Gln
			20					25						30

Asp	Pro	Phe	Glu	Lys	Cys	Met	Gln	Asp	Pro	Asp	Tyr	Glu	Gln	Leu
			35					40						45

Leu	Lys	Val	Val	Thr	Trp	Gly	Leu	Asn	Arg	Thr	Leu	Lys	Pro	Gln
			50					55						60

Arg	Val	Ile	Val	Val	Gly	Ala	Gly	Val	Ala	Gly	Leu	Val	Ala	Ala
			65					70						75

Lys	Val	Leu	Ser	Asp	Ala	Gly	His	Lys	Val	Thr	Ile	Leu	Glu	Ala
			80					85						90

Asp	Asn	Arg	Ile	Gly	Gly	Arg	Ile	Phe	Thr	Tyr	Arg	Asp	Gln	Asn
			95					100						105

Thr	Gly	Trp	Ile	Gly	Glu	Leu	Gly	Ala	Met	Arg	Met	Pro	Ser	Ser
			110					115						120

His	Arg	Ile	Leu	His	Lys	Leu	Cys	Gln	Gly	Leu	Gly	Leu	Asn	Leu
			125					130						135

Thr	Lys	Phe	Thr	Gln	Tyr	Asp	Lys	Asn	Thr	Trp	Thr	Glu	Val	His
			140					145						150

Glu	Val	Lys	Leu	Arg	Asn	Tyr	Val	Val	Glu	Lys	Val	Pro	Glu	Lys
			155					160						165

90

```
Leu Gly Tyr Ala Leu Arg Pro Gln Glu Lys Gly His Ser Pro Glu
            170                 175                 180

Asp Ile Tyr Gln Met Ala Leu Asn Gln Ala Leu Lys Asp Leu Lys
            185                 190                 195

Ala Leu Gly Cys Arg Lys Ala Met Lys Lys Phe Glu Arg His Thr
            200                 205                 210

Leu Leu Glu Tyr Leu Leu Gly Glu Gly Asn Leu Ser Arg Pro Ala
            215                 220                 225

Val Gln Leu Leu Gly Asp Val Met Ser Glu Asp Gly Phe Phe Tyr
            230                 235                 240

Leu Ser Phe Ala Glu Ala Leu Arg Ala His Ser Cys Leu Ser Asp
            245                 250                 255

Arg Leu Gln Tyr Ser Arg Ile Val Gly Gly Trp Asp Leu Leu Pro
            260                 265                 270

Arg Ala Leu Leu Ser Ser Leu Ser Gly Leu Val Leu Leu Asn Ala
            275                 280                 285

Pro Val Val Ala Met Thr Gln Gly Pro His Asp Val His Val Gln
            290                 295                 300

Ile Glu Thr Ser Pro Pro Ala Arg Asn Leu Lys Val Leu Lys Ala
            305                 310                 315

Asp Val Val Leu Leu Thr Ala Ser Gly Pro Ala Val Lys Arg Ile
            320                 325                 330

Thr Phe Ser Pro Pro Leu Pro Arg His Met Gln Glu Ala Leu Arg
            335                 340                 345

Arg Leu His Tyr Val Pro Ala Thr Lys Val Phe Leu Ser Phe Arg
            350                 355                 360

Arg Pro Phe Trp Arg Glu Glu His Ile Glu Gly Gly His Ser Asn
            365                 370                 375

Thr Asp Arg Pro Ser Arg Met Ile Phe Tyr Pro Pro Pro Arg Glu
            380                 385                 390

Gly Ala Leu Leu Leu Ala Ser Tyr Thr Trp Ser Asp Ala Ala Ala
            395                 400                 405

Ala Phe Ala Gly Leu Ser Arg Glu Glu Ala Leu Arg Leu Ala Leu
            410                 415                 420

Asp Asp Val Ala Ala Leu His Gly Pro Val Val Arg Gln Leu Trp
            425                 430                 435

Asp Gly Thr Gly Val Val Lys Arg Trp Ala Glu Asp Gln His Ser
            440                 445                 450

Gln Gly Gly Phe Val Val Gln Pro Pro Ala Leu Trp Gln Thr Glu
```

91

Lys Asp Asp Trp Thr Val Pro Tyr Gly Arg Ile Tyr Phe Ala Gly
                470   475   480

Glu His Thr Ala Tyr Pro His Gly Trp Val Glu Thr Ala Val Lys
                485   490   495

Ser Ala Leu Arg Ala Ala Ile Lys Ile Asn Ser Arg Lys Gly Pro
                500   505   510

Ala Ser Asp Thr Ala Ser Pro Glu Gly His Ala Ser Asp Met Glu
                515   520   525

Gly Gln Gly His Val His Gly Val Ala Ser Ser Pro Ser His Asp
                530   535   540

Leu Ala Lys Glu Glu Gly Ser His Pro Pro Val Gln Gly Gln Leu
                545   550   555

Ser Leu Gln Asn Thr Thr His Thr Arg Thr Ser His
                560   565

<210> 85
<211> 3316
<212> DNA
<213> Homo sapiens

<400> 85
ctgacatggc ctgactcggg acagctcaga gcagggcaga actggggaca 50

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tggaggaacc acgagcgagg gaagaaggac agggactcgt gtggcaggaa 150

gaactcagag ccgggaagcc cccattcact agaagcactg agagatgcgg 200

ccccctcgca gggtctgaat ttcctgctgc tgttcacaaa gatgcttttt 250

atctttaact ttttgttttc cccacttccg accccggcgt tgatctgcat 300

cctgacattt ggagctgcca tcttcttgtg gctgatcacc agacctcaac 350

ccgtcttacc tcttcttgac ctgaacaatc agtctgtggg aattgaggga 400

ggagcacgga aggggttttc ccagaagaac aatgacctaa caagttgctg 450

cttctcagat gccaagacta tgtatgaggt tttccaaaga ggactcgctg 500

tgtctgacaa tgggccctgc ttgggatata gaaaaccaaa ccagccctac 550

agatggctat cttacaaaca ggtgtctgat agagcagagt acctgggttc 600

ctgtctcttg cataaaggtt ataaatcatc accagaccag tttgtcggca 650

tctttgctca gaataggcca gagtggatca tctccgaatt ggcttgttac 700

acgtactcta tggtagctgt acctctgtat gacaccttgg gaccagaagc 750

92

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catcgtacat attgtcaaca aggctgatat cgccatggtg atctgtgaca 800

caccccaaaa ggcattggtg ctgataggga atgtagagaa aggcttcacc 850

ccgagcctga aggtgatcat ccttatggac ccctttgatg atgacctgaa 900

gcaaagaggg gagaagagtg gaattgagat cttatcccta tatgatgctg 950

agaacctagg caaagagcac ttcagaaaac ctgtgcctcc tagcccagaa 1000

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cagctgtgga gccagagttg gattcttcca aggggatatt cggttgctgg 1250

ctgacgacat gaagactttg aagcccacat tgtttcccgc ggtgcctcga 1300

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gaagaagttc ttgttgaagc tggctgtttc cagtaaattc aaagagcttc 1400

aaaagggtat catcaggcat gatagtttct gggacaagct catctttgca 1450

aagatccagg acagcctggg cggaagggtt cgtgtaattg tcactggagc 1500

tgcccccatg tccacttcag tcatgacatt cttccgggca gcaatgggat 1550

gtcaggtgta tgaagcttat ggtcaaacag aatgcacagg tggctgtaca 1600

tttacattac ctggggactg gacatcaggt cacgttgggg tgcccctggc 1650

ttgcaattac gtgaagctgg aagatgtggc tgacatgaac tactttacag 1700

tgaataatga aggagaggtc tgcatcaagg gtacaaacgt gttcaaagga 1750

tacctgaagg accctgagaa gacacaggaa gccctggaca gtgatggctg 1800

gcttcacaca ggagacattg gtcgctggct cccgaatgga actctgaaga 1850

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gcaccagaga agatagaaaa tatctacaac aggagtcaac cagtgttaca 1950

aattttttgta cacggggaga gcttacggtc atccttagta ggagtggtgg 2000

ttcctgacac agatgtactt ccctcatttg cagccaagct tggggtgaag 2050

ggctcctttg aggaactgtg ccaaaaccaa gttgtaaggg aagccatttt 2100

agaagacttg cagaaaattg ggaaagaaag tggccttaaa acttttgaac 2150

aggtcaaagc catttttctt catccagagc cattttccat tgaaaatggg 2200
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93

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ctcttgacac caacattgaa agcaaagcga ggagagcttt ccaaatactt 2250

tcggacccaa attgacagcc tgtatgagca catccaggat taggataagg 2300

tacttaagta cctgccggcc cactgtgcac tgcttgtgag aaaatggatt 2350

aaaaactatt cttacatttg ttttgccttt cctcctattt tttttttaacc 2400

tgttaaactc taaagccata gcttttgttt tatattgaga catataatgt 2450

gtaaacttag ttcccaaata aatcaatcct gtctttccca tcttcgatgt 2500

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tcttctactg ttcaaactaa gagattttta aattctgaaa aactgcttac 2750

aattcatgtt ttctagccac tccacaaacc actaaaattt tagtttttagc 2800

ctatcactca tgtcaatcat atctatgaga caaatgtctc cgatgctctt 2850

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atttcctaaa ctctctagtt agatatctga cttgggagta ttaaaaattg 2950

ggtctatgac atactgtcca aaaggaatgc tgttcttaaa gcattattta 3000

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gaagctgtgg gggaaggagt tgacaggtgg gcccagtgaa cttttccagt 3100

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acaggcaagc aagatgccca cacaacaggc ttattttctg tgaaggaacc 3200

aactgatctc ccccacccctt ggattagagt tcctgctcta ccttacccac 3250

agataacaca tgttgtttct acttgtaaat gtaaagtctt taaataaac 3300

tattacagat aaaaaa 3316
```

<210> 86
<211> 739
<212> PRT
<213> Homo ·sapiens

<400> 86
```
Met Asp Ala Leu Lys Pro Pro Cys Leu Trp Arg Asn His Glu Arg
 1               5                  10                  15

Gly Lys Lys Asp Arg Asp Ser Cys Gly Arg Lys Asn Ser Glu Pro
                20                  25                  30
```

94

```
Gly Ser Pro His Ser Leu Glu Ala Leu Arg Asp Ala Ala Pro Ser
            35                  40                      45

Gln Gly Leu Asn Phe Leu Leu Leu Phe Thr Lys Met Leu Phe Ile
            50                  55                      60

Phe Asn Phe Leu Phe Ser Pro Leu Pro Thr Pro Ala Leu Ile Cys
            65                  70                      75

Ile Leu Thr Phe Gly Ala Ala Ile Phe Leu Trp Leu Ile Thr Arg
            80                  85                      90

Pro Gln Pro Val Leu Pro Leu Leu Asp Leu Asn Asn Gln Ser Val
            95                  100                     105

Gly Ile Glu Gly Gly Ala Arg Lys Gly Val Ser Gln Lys Asn Asn
            110                 115                     120

Asp Leu Thr Ser Cys Cys Phe Ser Asp Ala Lys Thr Met Tyr Glu
            125                 130                     135

Val Phe Gln Arg Gly Leu Ala Val Ser Asp Asn Gly Pro Cys Leu
            140                 145                     150

Gly Tyr Arg Lys Pro Asn Gln Pro Tyr Arg Trp Leu Ser Tyr Lys
            155                 160                     165

Gln Val Ser Asp Arg Ala Glu Tyr Leu Gly Ser Cys Leu Leu His
            170                 175                     180

Lys Gly Tyr Lys Ser Ser Pro Asp Gln Phe Val Gly Ile Phe Ala
            185                 190                     195

Gln Asn Arg Pro Glu Trp Ile Ile Ser Glu Leu Ala Cys Tyr Thr
            200                 205                     210

Tyr Ser Met Val Ala Val Pro Leu Tyr Asp Thr Leu Gly Pro Glu
            215                 220                     225

Ala Ile Val His Ile Val Asn Lys Ala Asp Ile Ala Met Val Ile
            230                 235                     240

Cys Asp Thr Pro Gln Lys Ala Leu Val Leu Ile Gly Asn Val Glu
            245                 250                     255

Lys Gly Phe Thr Pro Ser Leu Lys Val Ile Ile Leu Met Asp Pro
            260                 265                     270

Phe Asp Asp Asp Leu Lys Gln Arg Gly Glu Lys Ser Gly Ile Glu
            275                 280                     285

Ile Leu Ser Leu Tyr Asp Ala Glu Asn Leu Gly Lys Glu His Phe
            290                 295                     300

Arg Lys Pro Val Pro Pro Ser Pro Glu Asp Leu Ser Val Ile Cys
            305                 310                     315

Phe Thr Ser Gly Thr Thr Gly Asp Pro Lys Gly Ala Met Ile Thr


                            95
```

His Gln Asn Ile Val Ser Asn Ala Ala Ala Phe Leu Lys Cys Val
                    335   340   345

Glu His Ala Tyr Glu Pro Thr Pro Asp Asp Val Ala Ile Ser Tyr
                    350   355   360

Leu Pro Leu Ala His Met Phe Glu Arg Ile Val Gln Ala Val Val
                    365   370   375

Tyr Ser Cys Gly Ala Arg Val Gly Phe Phe Gln Gly Asp Ile Arg
                    380   385   390

Leu Leu Ala Asp Asp Met Lys Thr Leu Lys Pro Thr Leu Phe Pro
                    395   400   405

Ala Val Pro Arg Leu Leu Asn Arg Ile Tyr Asp Lys Val Gln Asn
                    410   415   420

Glu Ala Lys Thr Pro Leu Lys Lys Phe Leu Leu Lys Leu Ala Val
                    425   430   435

Ser Ser Lys Phe Lys Glu Leu Gln Lys Gly Ile Ile Arg His Asp
                    440   445   450

Ser Phe Trp Asp Lys Leu Ile Phe Ala Lys Ile Gln Asp Ser Leu
                    455   460   465

Gly Gly Arg Val Arg Val Ile Val Thr Gly Ala Ala Pro Met Ser
                    470   475   480

Thr Ser Val Met Thr Phe Phe Arg Ala Ala Met Gly Cys Gln Val
                    485   490   495

Tyr Glu Ala Tyr Gly Gln Thr Glu Cys Thr Gly Gly Cys Thr Phe
                    500   505   510

Thr Leu Pro Gly Asp Trp Thr Ser Gly His Val Gly Val Pro Leu
                    515   520   525

Ala Cys Asn Tyr Val Lys Leu Glu Asp Val Ala Asp Met Asn Tyr
                    530   535   540

Phe Thr Val Asn Asn Glu Gly Glu Val Cys Ile Lys Gly Thr Asn
                    545   550   555

Val Phe Lys Gly Tyr Leu Lys Asp Pro Glu Lys Thr Gln Glu Ala
                    560   565   570

Leu Asp Ser Asp Gly Trp Leu His Thr Gly Asp Ile Gly Arg Trp
                    575   580   585

Leu Pro Asn Gly Thr Leu Lys Ile Ile Asp Arg Lys Lys Asn Ile
                    590   595   600

Phe Lys Leu Ala Gln Gly Glu Tyr Ile Ala Pro Glu Lys Ile Glu
                    605   610   615

```
Asn Ile Tyr Asn Arg Ser Gln Pro Val Leu Gln Ile Phe Val His
              620             625             630

Gly Glu Ser Leu Arg Ser Ser Leu Val Gly Val Val Val Pro Asp
              635             640             645

Thr Asp Val Leu Pro Ser Phe Ala Ala Lys Leu Gly Val Lys Gly
              650             655             660

Ser Phe Glu Glu Leu Cys Gln Asn Gln Val Val Arg Glu Ala Ile
              665             670             675

Leu Glu Asp Leu Gln Lys Ile Gly Lys Glu Ser Gly Leu Lys Thr
              680             685             690

Phe Glu Gln Val Lys Ala Ile Phe Leu His Pro Glu Pro Phe Ser
              695             700             705

Ile Glu Asn Gly Leu Leu Thr Pro Thr Leu Lys Ala Lys Arg Gly
              710             715             720

Glu Leu Ser Lys Tyr Phe Arg Thr Gln Ile Asp Ser Leu Tyr Glu
              725             730      .      735

His Ile Gln Asp
```

<210> 87
<211> 2725
<212> DNA
<213> Homo sapiens

<400> 87

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gcccgagcgg ggcccggggc ccctaagcca ttcctgaagt catgggctgg  100

ccaggacatt ggtgacccgc caatccggta tggacgactg gaagcccagc  150

cccctcatca agccctttgg ggctcggaag aagcggagct ggtaccttac  200

ctggaagtat aaactgacaa accagcgggc cctgcggaga ttctgtcaga  250

cagggGccgt gctttTcctg ctggtgactg tcattgtcaa tatcaagttg  300

atcctggaca ctcggcgagc catcagtgaa gccaatgaag acccagagcc  350

agagcaagac tatgatgagg ccctaggccg cctggagccc ccacggcgca  400

gaggcagtgg tccccggcgg gtcctggacg tagaggtgta ttcaagtcgc  450

agcaaagtat atgtggcagt ggatggcacc acggtgctgg aggatgaggc  500

ccgggagcag ggccgggggca tccatgtcat tgtcctcaac caggccacgg  550

gccacgtgat ggcaaaacgt gtgtttgaca cgtactcacc tcatgaggat  600

gaggccatgg tgctattcct caacatggta gcgcccggcc gagtgctcat  650
```

97

```
ctgcactgtc aaggatgagg gctccttcca cctcaaggac acagccaagg 700

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gacacatggg ccttcgtggg acgaaaagga ggtcctgtct tcggggagaa 800

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agacagatgt gccattgagc tcagcagaag aggcagagtg ccactgggca 900

gacacagagc tgaaccgtcg ccgccggcgc ttctgcagca aagttgaggg 950

ctatggaagt gtatgcagct gcaaggaccc cacacccatc gagttcagcc 1000

ctgacccact cccagacaac aaggtcctca atgtgcctgt ggctgtcatt 1050

gcagggaacc gacccaatta cctgtacagg atgctgcgct ctctgctttc 1100

agcccagggg gtgtctcctc agatgataac agttttcatt gacggctact 1150

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catactccca tcagcatcaa gaatgcccgc gtgtctcagc actacaaggc 1250

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ttctggaaga ggacctggac attgctgtgg attttttcag tttcctgagc 1350

caatccatcc acctactgga ggaggatgac agcctgtact gcatctctgc 1400

ctggaatgac caggggtatg aacacacggc tgaggaccca gcactactgt 1450

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tcatccctga cgtttcccga tcctaccact ttggcatcgt cggcctcaac 1650

atgaatggct actttcacga ggcctacttc aagaagcaca agttcaacac 1700

ggttccaggt gtccagctca ggaatgtgga cagtctgaag aaagaagctt 1750

atgaagtgga agttcacagg ctgctcagtg aggctgaggt tctggaccac 1800

agcaagaacc cttgtgaaga ctctttcctg ccagacacag agggccacac 1850

ctacgtggcc tttattcgaa tggagaaaga tgatgacttc accacctgga 1900

cccagcttgc caagtgcctc catatctggg acctggatgt gcgtggcaac 1950

catcggggcc tgtggagatt gtttcggaag aagaaccact tcctggtggt 2000

gggggtcccg gcttcccct actcagtgaa gaagccaccc tcagtcaccc 2050

caattttcct ggagccaccc ccaaaggagg agggagcccc aggagcccca 2100
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98

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gaacagacat gagacctcct ccaggaccct gcggggctgg gtactgtgta 2150

ccccaggct ggctagccct tccctccatc ctgtaggatt ttgtagatgc 2200

tggtaggggc tggggctacc ttgttttta catgagactt aattactaac 2250

tccaaggga gggttcccct gctccaacac cccgttcctg agttaaaagt 2300

ctatttattt acttccttgt tggagaaggg caggagagta cctgggaatc 2350

attacgatcc ctagcagctc atcctgccct ttgaataccc tcactttcca 2400

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aacaggccga acctggaggg cctggatttc tttttgggct ggaatgctgc 2500

cctgagggtg gggctggctc ttactcagga aactgctgtg cccaacccat 2550

ggacaggccc agctggggcc cacatgctga cacagactca ctcagagacc 2600

cttagacact ggaccaggcc tcctctcagc cttctctttg tccagatttc 2650

caaagctgga taagttggtc attgattaaa aaaggagaag ccctctggga 2700

aaaaaaaaaa aaaaaaaaaa aaaaa 2725
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<210> 88
<211> 660
<212> PRT
<213> Homo sapiens

<400> 88

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Met Asp Asp Trp Lys Pro Ser Pro Leu Ile Lys Pro Phe Gly Ala
1               5                  10                  15

Arg Lys Lys Arg Ser Trp Tyr Leu Thr Trp Lys Tyr Lys Leu Thr
                20                  25                  30

Asn Gln Arg Ala Leu Arg Arg Phe Cys Gln Thr Gly Ala Val Leu
                35                  40                  45

Phe Leu Leu Val Thr Val Ile Val Asn Ile Lys Leu Ile Leu Asp
                50                  55                  60

Thr Arg Arg Ala Ile Ser Glu Ala Asn Glu Asp Pro Glu Pro Glu
                65                  70                  75

Gln Asp Tyr Asp Glu Ala Leu Gly Arg Leu Glu Pro Pro Arg Arg
                80                  85                  90

Arg Gly Ser Gly Pro Arg Arg Val Leu Asp Val Glu Val Tyr Ser
                95                  100                 105

Ser Arg Ser Lys Val Tyr Val Ala Val Asp Gly Thr Thr Val Leu
                110                 115                 120

Glu Asp Glu Ala Arg Glu Gln Gly Arg Gly Ile His Val Ile Val
                125                 130                 135
```

99

Leu Asn Gln Ala Thr Gly His Val Met Ala Lys Arg Val Phe Asp
                140   145   150

Thr Tyr Ser Pro His Glu Asp Glu Ala Met Val Leu Phe Leu Asn
                155   160   165

Met Val Ala Pro Gly Arg Val Leu Ile Cys Thr Val Lys Asp Glu
                170   175   180

Gly Ser Phe His Leu Lys Asp Thr Ala Lys Ala Leu Leu Arg Ser
                185   190   195

Leu Gly Ser Gln Ala Gly Pro Ala Leu Gly Trp Arg Asp Thr Trp
                200   205   210

Ala Phe Val Gly Arg Lys Gly Gly Pro Val Phe Gly Glu Lys His
                215   220   225

Ser Lys Ser Pro Ala Leu Ser Ser Trp Gly Asp Pro Val Leu Leu
                230   235   240

Lys Thr Asp Val Pro Leu Ser Ser Ala Glu Glu Ala Glu Cys His
                245   250   255

Trp Ala Asp Thr Glu Leu Asn Arg Arg Arg Arg Arg Phe Cys Ser
                260   265   270

Lys Val Glu Gly Tyr Gly Ser Val Cys Ser Cys Lys Asp Pro Thr
                275   280   285

Pro Ile Glu Phe Ser Pro Asp Pro Leu Pro Asp Asn Lys Val Leu
                290   295   300

Asn Val Pro Val Ala Val Ile Ala Gly Asn Arg Pro Asn Tyr Leu
                305   310   315

Tyr Arg Met Leu Arg Ser Leu Leu Ser Ala Gln Gly Val Ser Pro
                320   325   330

Gln Met Ile Thr Val Phe Ile Asp Gly Tyr Tyr Glu Glu Pro Met
                335   340   345

Asp Val Val Ala Leu Phe Gly Leu Arg Gly Ile Gln His Thr Pro
                350   355   360

Ile Ser Ile Lys Asn Ala Arg Val Ser Gln His Tyr Lys Ala Ser
                365   370   375

Leu Thr Ala Thr Phe Asn Leu Phe Pro Glu Ala Lys Phe Ala Val
                380   385   390

Val Leu Glu Glu Asp Leu Asp Ile Ala Val Asp Phe Phe Ser Phe
                395   400   405

Leu Ser Gln Ser Ile His Leu Leu Glu Glu Asp Asp Ser Leu Tyr
                410   415   420

Cys Ile Ser Ala Trp Asn Asp Gln Gly Tyr Glu His Thr Ala Glu

100

```
                  425                      430                      435

      Asp Pro Ala Leu Leu Tyr Arg Val Glu Thr Met Pro Gly Leu Gly
                  440                      445                      450

      Trp Val Leu Arg Arg Ser Leu Tyr Lys Glu Glu Leu Glu Pro Lys
                  455                      460                      465

      Trp Pro Thr Pro Glu Lys Leu Trp Asp Trp Asp Met Trp Met Arg
                  470                      475                      480

      Met Pro Glu Gln Arg Arg Gly Arg Glu Cys Ile Ile Pro Asp Val
                  485                      490                      495

      Ser Arg Ser Tyr His Phe Gly Ile Val Gly Leu Asn Met Asn Gly
                  500                      505                      510

      Tyr Phe His Glu Ala Tyr Phe Lys Lys His Lys Phe Asn Thr Val
                  515                      520                      525

      Pro Gly Val Gln Leu Arg Asn Val Asp Ser Leu Lys Lys Glu Ala
                  530                      535                      540

      Tyr Glu Val Glu Val His Arg Leu Leu Ser Glu Ala Glu Val Leu
                  545                      550                      555

      Asp His Ser Lys Asn Pro Cys Glu Asp Ser Phe Leu Pro Asp Thr
                  560                      565                      570

      Glu Gly His Thr Tyr Val Ala Phe Ile Arg Met Glu Lys Asp Asp
                  575                      580                      585

      Asp Phe Thr Thr Trp Thr Gln Leu Ala Lys Cys Leu His Ile Trp
                  590                      595                      600

      Asp Leu Asp Val Arg Gly Asn His Arg Gly Leu Trp Arg Leu Phe
                  605                      610                      615

      Arg Lys Lys Asn His Phe Leu Val Val Gly Val Pro Ala Ser Pro
                  620                      625                      630

      Tyr Ser Val Lys Lys Pro Pro Ser Val Thr Pro Ile Phe Leu Glu
                  635                      640                      645

      Pro Pro Pro Lys Glu Glu Gly Ala Pro Gly Ala Pro Glu Gln Thr
                  650                      655                      660
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<210> 89
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-25
<223> Synthetic construct.

<400> 89

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   gatggcaaaa cgtgtgtttg acacg 25

<210> 90
<211> 22
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-22
<223> Synthetic construct.

<400> 90
  cctcaaccag gccacgggcc ac 22

<210> 91
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-24
<223> Synthetic construct.

<400> 91
  cccaggcaga gatgcagtac aggc 24

<210> 92
<211> 26
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-26
<223> Synthetic construct.

<400> 92
  cctccagtag gtggatggat tggctc 26

<210> 93
<211> 47
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-47
<223> Synthetic construct.

<400> 93
  ctcacctcat gaggatgagg ccatggtgct attcctcaac atggtag 47

<210> 94
<211> 3037
<212> DNA
<213> Homo sapiens
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<400> 94

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cggacgcgtg ggctgctggt gggaaggcct aaagaactgg aaagcccact 50

ctcttggaac caccacacct gtttaaagaa cctaagcacc atttaaagcc 100

actggaaatt tgttgtctag tggttgtggg tgaataaagg agggcagaat 150

ggatgatttc atctccatta gcctgctgtc tctggctatg ttggtgggat 200

gttacgtggc cggaatcatt cccttggctg ttaatttctc agaggaacga 250

ctgaagctgg tgactgtttt gggtgctggc cttctctgtg gaactgctct 300

ggcagtcatc gtgcctgaag gagtacatgc cctttatgaa gatattcttg 350

agggaaaaca ccaccaagca agtgaaacac ataatgtgat tgcatcagac 400

aaagcagcag aaaaatcagt tgtccatgaa catgagcaca gccacgacca 450

cacacagctg catgcctata ttggtgtttc cctcgttctg ggcttcgttt 500

tcatgttgct ggtggaccag attggtaact cccatgtgca ttctactgac 550

gatccagaag cagcaaggtc tagcaattcc aaaatcacca ccacgctggg 600

tctggttgtc catgctgcag ctgatggtgt tgctttggga gcagcagcat 650

ctacttcaca gaccagtgtc cagttaattg tgtttgtggc aatcatgcta 700

cataaggcac cagctgcttt tggactggtt tccttcttga tgcatgctgg 750

cttagagcgg aatcgaatca gaaagcactt gctggtcttt gcattggcag 800

caccagttat gtccatggtg acatacttag gactgagtaa gagcagtaaa 850

gaagcccttt cagaggtgaa cgccacggga gtggccatgc ttttctctgc 900

cgggacattt ctttatgttg ccacagtaca tgtcctccct gaggtgggcg 950

gaatagggca cagccacaag cccgatgcca cgggagggag aggcctcagc 1000

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gaggggaggt gaggttaaaa cctgagtaat ggaaaagctt ttagagtaga 1250

aacacattta cgttgcagtt agctatagac atcccattgt gttatctttt 1300

aaaaggccct tgacattttg cgttttaata tttctcttaa ccctattctc 1350

agggaagatg gaatttagtt ttaaggaaaa gaggagaact tcatactcac 1400

aatgaaatag tgattatgaa aatacagtgt tctgtaatta agctatgtct 1450
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103

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ctttcttctt agtttagagg ctctgctact ttatccattg attttttaaca 1500

tggttcccac catgtaagac tggtgcttta gcatctatgc cacatgcgtt 1550

gatggaaggt catagcaccc actcacttag atgctaaagg tgattctagt 1600

taatctggga ttagggtcag gaaaatgata gcaagacaca ttgaaagctc 1650

tctttatact caaaagagat atccattgaa aagggatgtc tagagggatt 1700

taaacagctc ctttggcacg tgcctctctg aatccagcct gccattccat 1750

caaatggagc aggagaggtg ggaggagctt ctaaagaggt gactggtatt 1800

ttgtagcatt ccttgtcaag ttctcctttg cagaatacct gtctccacat 1850

tcctagagag gagccaagtt ctagtagttt cagttctagg ctttccttca 1900

agaacagtca gatcacaaag tgtctttgga aattaaggga tattaaattt 1950

taagtgattt ttggatggtt attgatatct ttgtagtagc ttttttttaaa 2000

agactaccaa aatgtatggt tgtcctttt ttttgttttt tttttttta 2050

attatttctc ttagcagatc agcaatccct ctagggacct aaatactagg 2100

tcagctttgg cgacactgtg tcttctcaca taaccacctg tagcaagatg 2150

gatcataaat gagaagtgtt tgcctattga tttaaagctt attggaatca 2200

tgtctcttgt ctcttcgtct tttctttgct tttcttctaa cttttccctc 2250

tagcctctcc tcgccacaat ttgctgctta ctgctggtgt taatatttgt 2300

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caaatgccgc tttgttgagc ccttaaaata ccacctcctc atgtgtaaat 2450

tgacacaatc actaatctgg taatttaaac aattgagata gcaaaagtgt 2500

ttaacagact aggataattt ttttttcata tttgccaaaa tttttgtaaa 2550

ccctgtcttg tcaaataagt gtataatatt gtattattaa tttattttta 2600

ctttctatac catttcaaaa cacattacac taaggggaa ccaagactag 2650

tttcttcagg gcagtggacg tagtagtttg taaaaacgtt ttctatgacg 2700

cataagctag catgcctatg atttatttcc ttcatgaatt tgtcactgga 2750

tcagcagctg tggaaataaa gcttgtgagc cctctgctgg ccacagtgag 2800

gaaagtagca caaataggat acagttgtat gtagtcattg gcaacaattg 2850

catacaattt tactaccaag agaaggtata gtatggaaag tccaaatgac 2900
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104

ttccttgatt ggatgttaac agctgactgg tgtgagactt gaggtttcat 2950

ctagtccttc aaaactatat ggttgcctag attctctctg gaaactgact 3000

ttgtcaaata aatagcagat tgtagtgtca aaaaaaa 3037

<210> 95
<211> 307
<212> PRT
<213> Homo sapiens

<400> 95

Met Asp Asp Phe Ile Ser Ile Ser Leu Leu Ser Leu Ala Met Leu
1   5   10   15

Val Gly Cys Tyr Val Ala Gly Ile Ile Pro Leu Ala Val Asn Phe
                20   25   30

Ser Glu Glu Arg Leu Lys Leu Val Thr Val Leu Gly Ala Gly Leu
                35   40   45

Leu Cys Gly Thr Ala Leu Ala Val Ile Val Pro Glu Gly Val His
                50   55   60

Ala Leu Tyr Glu Asp Ile Leu Glu Gly Lys His His Gln Ala Ser
                65   70   75

Glu Thr His Asn Val Ile Ala Ser Asp Lys Ala Ala Glu Lys Ser
                80   85   90

Val Val His Glu His Glu His Ser His Asp His Thr Gln Leu His
                95   100   105

Ala Tyr Ile Gly Val Ser Leu Val Leu Gly Phe Val Phe Met Leu
                110   115   120

Leu Val Asp Gln Ile Gly Asn Ser His Val His Ser Thr Asp Asp
                125   130   135

Pro Glu Ala Ala Arg Ser Ser Asn Ser Lys Ile Thr Thr Thr Leu
                140   145   150

Gly Leu Val Val His Ala Ala Ala Asp Gly Val Ala Leu Gly Ala
                155   160   165

Ala Ala Ser Thr Ser Gln Thr Ser Val Gln Leu Ile Val Phe Val
                170   175   180

Ala Ile Met Leu His Lys Ala Pro Ala Ala Phe Gly Leu Val Ser
                185   190   195

Phe Leu Met His Ala Gly Leu Glu Arg Asn Arg Ile Arg Lys His
                200   205   210

Leu Leu Val Phe Ala Leu Ala Ala Pro Val Met Ser Met Val Thr
                215   220   225

Tyr Leu Gly Leu Ser Lys Ser Ser Lys Glu Ala Leu Ser Glu Val

105

```
    Asn Ala Thr Gly Val Ala Met Leu Phe Ser Ala Gly Thr Phe Leu
                    245                 250                 255

    Tyr Val Ala Thr Val His Val Leu Pro Glu Val Gly Gly Ile Gly
                    260                 265                 270

    His Ser His Lys Pro Asp Ala Thr Gly Gly Arg Gly Leu Ser Arg
                    275                 280                 285

    Leu Glu Val Ala Ala Leu Val Leu Gly Cys Leu Ile Pro Leu Ile
                    290                 295                 300

    Leu Ser Val Gly His Gln His
                    305
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<210> 96
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-25
<223> Synthetic construct.

<400> 96
 gttgtgggtg aataaaggag ggcag 25

<210> 97
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-25
<223> Synthetic construct.

<400> 97
 ctgtgctcat gttcatggac aactg 25

<210> 98
<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-50
<223> Synthetic construct.

<400> 98
 ggatgatttc atctccatta gcctgctgtc tctggctatg ttggtgggat 50

<210> 99
<211> 1429
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<212> DNA
<213> Homo sapiens

<400> 99
gctcgaggcc ggcggcggcg ggagagcgac ccgggcggcc tcgtagcggg 50

gccccggatc cccgagtggc ggccggagcc tcgaaaagag attctcagcg 100

ctgattttga gatgatgggc ttgggaaacg ggcgtcgcag catgaagtcg 150

ccgcccctcg tgctggccgc cctggtggcc tgcatcatcg tcttgggctt 200

caactactgg attgcgagct cccggagcgt ggacctccag acacggatca 250

tggagctgga aggcagggtc cgcagggcgg ctgcagagag aggcgccgtg 300

gagctgaaga agaacgagtt ccagggagag ctggagaagc agcgggagca 350

gcttgacaaa atccagtcca gccacaactt ccagctggag agcgtcaaca 400

agctgtacca ggacgaaaag gcggttttgg tgaataacat caccacaggt 450

gagaggctca tccgagtgct gcaagaccag ttaaagaccc tgcagaggaa 500

ttacggcagg ctgcagcagg atgtcctcca gtttcagaag aaccagacca 550

acctggagag gaagttctcc tacgacctga gccagtgcat caatcagatg 600

aaggaggtga aggaacagtg tgaggagcga atagaagagg tcaccaaaaa 650

ggggaatgaa gctgtagctt ccagagacct gagtgaaaac aacgaccaga 700

gacagcagct ccaagccctc agtgagcctc agcccaggct gcaggcagca 750

ggcctgccac acacagaggt gccacaaggg aagggaaacg tgcttggtaa 800

cagcaagtcc cagacaccag cccccagttc cgaagtggtt ttggattcaa 850

agagacaagt tgagaaagag gaaaccaatg agatccaggt ggtgaatgag 900

gagcctcaga gggacaggct gccgcaggag ccaggccggg agcaggtggt 950

ggaagacaga cctgtaggtg gaagaggctt cggggggagcc ggagaactgg 1000

gccagacccc acaggtgcag gctgccctgt cagtgagcca ggaaaatcca 1050

gagatggagg gccctgagcg agaccagctt gtcatccccg acggacagga 1100

ggaggagcag gaagctgccg gggaagggag aaaccagcag aaactgagag 1150

gagaagatga ctacaacatg gatgaaaatg aagcagaatc tgagacagac 1200

aagcaagcag ccctggcagg gaatgacaga aacatagatg tttttaatgt 1250

tgaagatcag aaaagagaca ccataaattt acttgatcag cgtgaaaagc 1300

ggaatcatac actctgaatt gaactggaat cacatatttc acaacagggc 1350

107

cgaagagatg actataaaat gttcatgagg gactgaatac tgaaaactgt 1400

gaaatgtact aaataaaatg tacatctga 1429

<210> 100
<211> 401
<212> PRT
<213> Homo sapiens

<400> 100
Met Met Gly Leu Gly Asn Gly Arg Arg Ser Met Lys Ser Pro Pro
1   5   10   15

Leu Val Leu Ala Ala Leu Val Ala Cys Ile Ile Val Leu Gly Phe
                20   25   30

Asn Tyr Trp Ile Ala Ser Ser Arg Ser Val Asp Leu Gln Thr Arg
                35   40   45

Ile Met Glu Leu Glu Gly Arg Val Arg Arg Ala Ala Ala Glu Arg
                50   55   60

Gly Ala Val Glu Leu Lys Lys Asn Glu Phe Gln Gly Glu Leu Glu
                65   70   75

Lys Gln Arg Glu Gln Leu Asp Lys Ile Gln Ser Ser His Asn Phe
                80   85   90

Gln Leu Glu Ser Val Asn Lys Leu Tyr Gln Asp Glu Lys Ala Val
                95   100   105

Leu Val Asn Asn Ile Thr Thr Gly Glu Arg Leu Ile Arg Val Leu
                110   115   120

Gln Asp Gln Leu Lys Thr Leu Gln Arg Asn Tyr Gly Arg Leu Gln
                125   130   135

Gln Asp Val Leu Gln Phe Gln Lys Asn Gln Thr Asn Leu Glu Arg
                140   145   150

Lys Phe Ser Tyr Asp Leu Ser Gln Cys Ile Asn Gln Met Lys Glu
                155   160   165

Val Lys Glu Gln Cys Glu Glu Arg Ile Glu Glu Val Thr Lys Lys
                170   175   180

Gly Asn Glu Ala Val Ala Ser Arg Asp Leu Ser Glu Asn Asn Asp
                185   190   195

Gln Arg Gln Gln Leu Gln Ala Leu Ser Glu Pro Gln Pro Arg Leu
                200   205   210

Gln Ala Ala Gly Leu Pro His Thr Glu Val Pro Gln Gly Lys Gly
                215   220   225

Asn Val Leu Gly Asn Ser Lys Ser Gln Thr Pro Ala Pro Ser Ser
                230   235   240

108

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Glu Val Val Leu Asp Ser Lys Arg Gln Val Glu Lys Glu Glu Thr
              245                 250                 255

Asn Glu Ile Gln Val Val Asn Glu Glu Pro Gln Arg Asp Arg Leu
              260                 265                 270

Pro Gln Glu Pro Gly Arg Glu Gln Val Val Glu Asp Arg Pro Val
              275                 280                 285

Gly Gly Arg Gly Phe Gly Gly Ala Gly Glu Leu Gly Gln Thr Pro
              290                 295                 300

Gln Val Gln Ala Ala Leu Ser Val Ser Gln Glu Asn Pro Glu Met
              305                 310                 315

Glu Gly Pro Glu Arg Asp Gln Leu Val Ile Pro Asp Gly Gln Glu
              320                 325                 330

Glu Glu Gln Glu Ala Ala Gly Glu Gly Arg Asn Gln Gln Lys Leu
              335                 340                 345

Arg Gly Glu Asp Asp Tyr Asn Met Asp Glu Asn Glu Ala Glu Ser
              350                 355                 360

Glu Thr Asp Lys Gln Ala Ala Leu Ala Gly Asn Asp Arg Asn Ile
              365                 370                 375

Asp Val Phe Asn Val Glu Asp Gln Lys Arg Asp Thr Ile Asn Leu
              380                 385                 390

Leu Asp Gln Arg Glu Lys Arg Asn His Thr Leu
              395                 400

<210> 101
<211> 3671
<212> DNA
<213> Homo sapiens

<400> 101
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ttctacgctg gcattgccct cttcaccagt ggcttcctgc tcacccgttt 100

ggagctcacc aaccatagca gctgccaaga gccccaggc cctgggtccc 150

tgccatgggg gagccaaggg aaacctgggg cctgctggat ggcttcccga 200

ttttcgcggg ttgtgttggt gctgatagat gctctgcgat ttgacttcgc 250

ccagccccag cattcacacg tgcctagaga gcctcctgtc tccctaccct 300

tcctgggcaa actaagctcc ttgcagagga tcctggagat tcagccccac 350

catgcccggc tctaccgatc tcaggttgac cctcctacca ccaccatgca 400

gcgcctcaag gccctcacca ctggctcact gcctaccttt attgatgctg 450

gtagtaactt cgccagccac gccatagtgg aagacaatct cattaagcag 500
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109

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ctcaccagtg caggaaggcg tgtagtcttc atgggagatg atacctggaa 550

agaccttttc cctggtgctt tctccaaagc tttcttcttc ccatccttca 600

atgtcagaga cctagacaca gtggacaatg gcatcctgga acacctctac 650

cccaccatgg acagtggtga atgggacgtg ctgattgctc acttcctggg 700

tgtggaccac tgtggccaca agcatggccc tcaccaccct gaaatggcca 750

agaaacttag ccagatggac caggtgatcc agggacttgt ggagcgtctg 800

gagaatgaca cactgctggt agtggctggg gaccatggga tgaccacaaa 850

tggagaccat ggaggggaca gtgagctgga ggtctcagct gctctctttc 900

tgtatagccc cacagcagtc ttccccagca ccccaccaga ggagccagag 950

gtgattcctc aagttagcct tgtgcccacg ctggccctgc tgctgggcct 1000

gcccatccca tttgggaata tcggggaagt gatggctgag ctattctcag 1050

ggggtgagga ctcccagccc cactcctctg ctttagccca agcctcagct 1100

ctccatctca atgctcagca ggtgtcccga tttcttcata cctactcagc 1150

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cctgacacct gtggcctggg gcctggttgg ggccatagcg tatgctggac 1500

tcctgggaac tattgagctg aagctagatc tagtgcttct aggggctgtg 1550

gctgcagtga gctcattcct ccctttttctg tggaaagcct gggctggctg 1600

ggggtccaag aggcccctgg caaccctgtt tcccatccct gggcccgtcc 1650

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gctagctggg cttttttcatc gttgccctga agagacacct gtttgccact 1950
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110

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cctctccctg gctgagtcct ctggcatcca tggtgggtgg tcgagccaag 2000

aatttatggt atggagcttg tgtggcggcg ctggtggccc tgttagctgc 2050

cgtgcgcttg tggcttcgcc gctatggtaa tctcaagagc cccgagccac 2100

ccatgctctt tgtgcgctgg ggactgcccc taatggcatt gggtactgct 2150

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gtgaaggctg gggcaggcgc tccaaggacc aggactgtcc tcactccctt 2350

ctcaggcccc cccacttctc aagctgactt ggattatgtg gtccctcaaa 2400

tctaccgaca catgcaggag gagttccggg gccggttaga gaggaccaaa 2450

tctcagggtc ccctgactgt ggctgcttat cagttgggga gtgtctactc 2500

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cacagacctt ctactccaca ggccaccagc ctgtctttcc agccatccat 2750

tggcatgcag ccttcgtggg attcccagag ggtcatggct cctgtacttg 2800

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ctctttatcc ttggtattca gattctggcc tgtgccttgg cagcctccat 3100

ccttcgcagg catctcatgg tctggaaagt gtttgcccct aagttcatat 3150

ttgaggctgt gggcttcatt gtgagcagcg tgggacttct cctgggcata 3200

gctttggtga tgagagtgga tggtgctgtg agctcctggt tcaggcagct 3250

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acagagagtg ctggagaaca gtgtagcctg gcctgtacag gtactggatg 3350

atctgcaaga caggctcagc catactctta ctatcatgca gccaggggcc 3400
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111

gctgacatct aggacttcat tattctataa ttcaggacca cagtggagta 3450

tgatccctaa ctcctgattt ggatgcatct gagggacaag ggggggcggtc 3500

tccgaagtgg aataaaatag gccgggcgtg gtgacttgca cctataatcc 3550

cagcactttg ggaggcagag gtgggaggat tgcttggtcc caggagttca 3600

agaccagcct gtggaacata acaagacccc gtctctacta tttaaaaaaa 3650

agtgtaataa aatgataata t 3671

<210> 102
<211> 1089
<212> PRT
<213> Homo sapiens

<400> 102
Met Gln Lys Ala Ser Val Leu Leu Phe Leu Ala Trp Val Cys Phe
1   5   10   15

Leu Phe Tyr Ala Gly Ile Ala Leu Phe Thr Ser Gly Phe Leu Leu
                20   25   30

Thr Arg Leu Glu Leu Thr Asn His Ser Ser Cys Gln Glu Pro Pro
                35   40   45

Gly Pro Gly Ser Leu Pro Trp Gly Ser Gln Gly Lys Pro Gly Ala
                50   55   60

Cys Trp Met Ala Ser Arg Phe Ser Arg Val Val Leu Val Leu Ile
                65   70   75

Asp Ala Leu Arg Phe Asp Phe Ala Gln Pro Gln His Ser His Val
                80   85   90

Pro Arg Glu Pro Pro Val Ser Leu Pro Phe Leu Gly Lys Leu Ser
                95   100   105

Ser Leu Gln Arg Ile Leu Glu Ile Gln Pro His His Ala Arg Leu
                110   115   120

Tyr Arg Ser Gln Val Asp Pro Pro Thr Thr Thr Met Gln Arg Leu
                125   130   135

Lys Ala Leu Thr Thr Gly Ser Leu Pro Thr Phe Ile Asp Ala Gly
                140   145   150

Ser Asn Phe Ala Ser His Ala Ile Val Glu Asp Asn Leu Ile Lys
                155   160   165

Gln Leu Thr Ser Ala Gly Arg Arg Val Val Phe Met Gly Asp Asp
                170   175   180

Thr Trp Lys Asp Leu Phe Pro Gly Ala Phe Ser Lys Ala Phe Phe
                185   190   195

Phe Pro Ser Phe Asn Val Arg Asp Leu Asp Thr Val Asp Asn Gly

112

```
                200                    205                    210
Ile Leu Glu His Leu Tyr Pro Thr Met Asp Ser Gly Glu Trp Asp
                215                    220                    225
Val Leu Ile Ala His Phe Leu Gly Val Asp His Cys Gly His Lys
                230                    235                    240
His Gly Pro His His Pro Glu Met Ala Lys Lys Leu Ser Gln Met
                245                    250                    255
Asp Gln Val Ile Gln Gly Leu Val Glu Arg Leu Glu Asn Asp Thr
                260                    265                    270
Leu Leu Val Val Ala Gly Asp His Gly Met Thr Thr Asn Gly Asp
                275                    280                    285
His Gly Gly Asp Ser Glu Leu Glu Val Ser Ala Ala Leu Phe Leu
                290                    295                    300
Tyr Ser Pro Thr Ala Val Phe Pro Ser Thr Pro Pro Glu Glu Pro
                305                    310                    315
Glu Val Ile Pro Gln Val Ser Leu Val Pro Thr Leu Ala Leu Leu
                320                    325                    330
Leu Gly Leu Pro Ile Pro Phe Gly Asn Ile Gly Glu Val Met Ala
                335                    340                    345
Glu Leu Phe Ser Gly Gly Glu Asp Ser Gln Pro His Ser Ser Ala
                350                    355                    360
Leu Ala Gln Ala Ser Ala Leu His Leu Asn Ala Gln Gln Val Ser
                365                    370                    375
Arg Phe Leu His Thr Tyr Ser Ala Ala Thr Gln Asp Leu Gln Ala
                380                    385                    390
Lys Glu Leu His Gln Leu Gln Asn Leu Phe Ser Lys Ala Ser Ala
                395                    400                    405
Asp Tyr Gln Trp Leu Leu Gln Ser Pro Lys Gly Ala Glu Ala Thr
                410                    415                    420
Leu Pro Thr Val Ile Ala Glu Leu Gln Gln Phe Leu Arg Gly Ala
                425                    430                    435
Arg Ala Met Cys Ile Glu Ser Trp Ala Arg Phe Ser Leu Val Arg
                440                    445                    450
Met Ala Gly Gly Thr Ala Leu Leu Ala Ala Ser Cys Phe Ile Cys
                455                    460                    465
Leu Leu Ala Ser Gln Trp Ala Ile Ser Pro Gly Phe Pro Phe Cys
                470                    475                    480
Pro Leu Leu Leu Thr Pro Val Ala Trp Gly Leu Val Gly Ala Ile
                485                    490                    495
```

113

```
Ala Tyr Ala Gly Leu Leu Gly Thr Ile Glu Leu Lys Leu Asp Leu
              500             505             510

Val Leu Leu Gly Ala Val Ala Ala Val Ser Ser Phe Leu Pro Phe
              515             520             525

Leu Trp Lys Ala Trp Ala Gly Trp Gly Ser Lys Arg Pro Leu Ala
              530             535             540

Thr Leu Phe Pro Ile Pro Gly Pro Val Leu Leu Leu Leu Leu Phe
              545             550             555

Arg Leu Ala Val Phe Phe Ser Asp Ser Phe Val Val Ala Glu Ala
              560             565             570

Arg Ala Thr Pro Phe Leu Leu Gly Ser Phe Ile Leu Leu Leu Val
              575             580             585

Val Gln Leu His Trp Glu Gly Gln Leu Leu Pro Pro Lys Leu Leu
              590             595             600

Thr Met Pro Arg Leu Gly Thr Ser Ala Thr Thr Asn Pro Pro Arg
              605             610             615

His Asn Gly Ala Tyr Ala Leu Arg Leu Gly Ile Gly Leu Leu Leu
              620             625             630

Cys Thr Arg Leu Ala Gly Leu Phe His Arg Cys Pro Glu Glu Thr
              635             640             645

Pro Val Cys His Ser Ser Pro Trp Leu Ser Pro Leu Ala Ser Met
              650             655             660

Val Gly Gly Arg Ala Lys Asn Leu Trp Tyr Gly Ala Cys Val Ala
              665             670             675

Ala Leu Val Ala Leu Leu Ala Ala Val Arg Leu Trp Leu Arg Arg
              680             685             690

Tyr Gly Asn Leu Lys Ser Pro Glu Pro Pro Met Leu Phe Val Arg
              695             700             705

Trp Gly Leu Pro Leu Met Ala Leu Gly Thr Ala Ala Tyr Trp Ala
              710             715             720

Leu Ala Ser Gly Ala Asp Glu Ala Pro Pro Arg Leu Arg Val Leu
              725             730             735

Val Ser Gly Ala Ser Met Val Leu Pro Arg Ala Val Ala Gly Leu
              740             745             750

Ala Ala Ser Gly Leu Ala Leu Leu Leu Trp Lys Pro Val Thr Val
              755             760             765

Leu Val Lys Ala Gly Ala Gly Ala Pro Arg Thr Arg Thr Val Leu
              770             775             780

Thr Pro Phe Ser Gly Pro Pro Thr Ser Gln Ala Asp Leu Asp Tyr
```

114

Val Val Pro Gln Ile Tyr Arg His Met Gln Glu Glu Phe Arg Gly
　　　　　　　800　　　　　　　805　　　　　　　810

Arg Leu Glu Arg Thr Lys Ser Gln Gly Pro Leu Thr Val Ala Ala
　　　　　　　815　　　　　　　820　　　　　　　825

Tyr Gln Leu Gly Ser Val Tyr Ser Ala Ala Met Val Thr Ala Leu
　　　　　　　830　　　　　　　835　　　　　　　840

Thr Leu Leu Ala Phe Pro Leu Leu Leu His Ala Glu Arg Ile
　　　　　　　845　　　　　　　850　　　　　　　855

Ser Leu Val Phe Leu Leu Leu Phe Leu Gln Ser Phe Leu Leu Leu
　　　　　　　860　　　　　　　865　　　　　　　870

His Leu Leu Ala Ala Gly Ile Pro Val Thr Thr Pro Gly Pro Phe
　　　　　　　875　　　　　　　880　　　　　　　885

Thr Val Pro Trp Gln Ala Val Ser Ala Trp Ala Leu Met Ala Thr
　　　　　　　890　　　　　　　895　　　　　　　900

Gln Thr Phe Tyr Ser Thr Gly His Gln Pro Val Phe Pro Ala Ile
　　　　　　　905　　　　　　　910　　　　　　　915

His Trp His Ala Ala Phe Val Gly Phe Pro Glu Gly His Gly Ser
　　　　　　　920　　　　　　　925　　　　　　　930

Cys Thr Trp Leu Pro Ala Leu Leu Val Gly Ala Asn Thr Phe Ala
　　　　　　　935　　　　　　　940　　　　　　　945

Ser His Leu Leu Phe Ala Val Gly Cys Pro Leu Leu Leu Leu Trp
　　　　　　　950　　　　　　　955　　　　　　　960

Pro Phe Leu Cys Glu Ser Gln Gly Leu Arg Lys Arg Gln Gln Pro
　　　　　　　965　　　　　　　970　　　　　　　975

Pro Gly Asn Glu Ala Asp Ala Arg Val Arg Pro Glu Glu Glu Glu
　　　　　　　980　　　　　　　985　　　　　　　990

Glu Pro Leu Met Glu Met Arg Leu Arg Asp Ala Pro Gln His Phe
　　　　　　　995　　　　　　　1000　　　　　　　1005

Tyr Ala Ala Leu Leu Gln Leu Gly Leu Lys Tyr Leu Phe Ile Leu
　　　　　　　1010　　　　　　　1015　　　　　　　1020

Gly Ile Gln Ile Leu Ala Cys Ala Leu Ala Ala Ser Ile Leu Arg
　　　　　　　1025　　　　　　　1030　　　　　　　1035

Arg His Leu Met Val Trp Lys Val Phe Ala Pro Lys Phe Ile Phe
　　　　　　　1040　　　　　　　1045　　　　　　　1050

Glu Ala Val Gly Phe Ile Val Ser Ser Val Gly Leu Leu Leu Gly
　　　　　　　1055　　　　　　　1060　　　　　　　1065

Ile Ala Leu Val Met Arg Val Asp Gly Ala Val Ser Ser Trp Phe
　　　　　　　1070　　　　　　　1075　　　　　　　1080

Arg Gln Leu Phe Leu Ala Gln Gln Arg
                    1085

<210> 103
<211> 1743
<212> DNA
<213> Homo sapiens

<400> 103
 tgccgctgcc gccgctgctg ctgttgctcc tggcggcgcc ttggggacgg 50

 gcagttccct gtgtctctgg tggtttgcct aaacctgcaa acatcacctt 100

 cttatccatc aacatgaaga atgtcctaca atggactcca ccagagggtc 150

 ttcaaggagt taaagttact tacactgtgc agtatttcat cacaaattgg 200

 cccaccagag gtggcactga ctacagatga gaagtccatt tctgttgtcc 250

 tgacagctcc agagaagtgg aagagaaatc cagaagacct tcctgtttcc 300

 atgcaacaaa tatactccaa tctgaagtat aacgtgtctg tgttgaatac 350

 taaatcaaac agaacgtggt cccagtgtgt gaccaaccac acgctggtgc 400

 tcacctggct ggagccgaac actctttact gcgtacacgt ggagtccttc 450

 gtcccagggc cccctcgccg tgctcagcct tctgagaagc agtgtgccag 500

 gactttgaaa gatcaatcat cagagttcaa ggctaaaatc atcttctggt 550

 atgttttgcc catatctatt accgtgtttc tttttttctgt gatgggctat 600

 tccatctacc gatatatcca cgttggcaaa gagaaacacc cagcaaattt 650

 gattttgatt tatggaaatg aatttgacaa aagattcttt gtgcctgctg 700

 aaaaaatcgt gattaacttt atcaccctca atatctcgga tgattctaaa 750

 atttctcatc aggatatgag tttactggga aaaagcagtg atgtatccag 800

 ccttaatgat cctcagccca gcgggaacct gaggcccct caggaggaag 850

 aggaggtgaa acatttaggg tatgcttcgc atttgatgga aatttttgt 900

 gactctgaag aaaacacgga aggtacttct ctcacccagc aagagtccct 950

 cagcagaaca atacccccgg ataaaacagt cattgaatat gaatatgatg 1000

 tcagaaccac tgacatttgt gcggggcctg aagagcagga gctcagtttg 1050

 caggaggagg tgtccacaca aggaacatta ttggagtcgc aggcagcgtt 1100

 ggcagtcttg ggccgcaaa cgttacagta ctcatacacc cctcagctcc 1150

 aagacttaga cccctggcg caggagcaca cagactcgga ggagggccg 1200

 gaggaagagc catcgacgac cctggtcgac tgggatcccc aaactggcag 1250

116

```
gctgtgtatt ccttcgctgt ccagcttcga ccaggattca gagggctgcg 1300

agccttctga gggggatggg ctcggagagg aggtcttct atctagactc 1350

tatgaggagc cggctccaga caggccacca ggagaaaatg aaacctatct 1400

catgcaattc atggaggaat gggggttata tgtgcagatg gaaaactgat 1450

gccaacactt ccttttgcct tttgtttcct gtgcaaacaa gtgagtcacc 1500

cctttgatcc cagccataaa gtacctggga tgaaagaagt tttttccagt 1550

ttgtcagtgt ctgtgagaat tacttatttc ttttctctat tctcatagca 1600

cgtgtgtgat tggttcatgc atgtaggtct cttaacaatg atggtgggcc 1650

tctggagtcc aggggctggc cggttgttct atgcagagaa agcagtcaat 1700

aaatgtttgc cagactgggt gcagaattta ttcaggtggg tgt 1743
```

<210> 104
<211> 442
<212> PRT
<213> Homo sapiens

<400> 104

```
Met Ser Tyr Asn Gly Leu His Gln Arg Val Phe Lys Glu Leu Lys
 1               5                  10                  15

Leu Leu Thr Leu Cys Ser Ile Ser Ser Gln Ile Gly Pro Pro Glu
                20                  25                  30

Val Ala Leu Thr Thr Asp Glu Lys Ser Ile Ser Val Val Leu Thr
                35                  40                  45

Ala Pro Glu Lys Trp Lys Arg Asn Pro Glu Asp Leu Pro Val Ser
                50                  55                  60

Met Gln Gln Ile Tyr Ser Asn Leu Lys Tyr Asn Val Ser Val Leu
                65                  70                  75

Asn Thr Lys Ser Asn Arg Thr Trp Ser Gln Cys Val Thr Asn His
                80                  85                  90

Thr Leu Val Leu Thr Trp Leu Glu Pro Asn Thr Leu Tyr Cys Val
                95                  100                 105

His Val Glu Ser Phe Val Pro Gly Pro Pro Arg Arg Ala Gln Pro
                110                 115                 120

Ser Glu Lys Gln Cys Ala Arg Thr Leu Lys Asp Gln Ser Ser Glu
                125                 130                 135

Phe Lys Ala Lys Ile Ile Phe Trp Tyr Val Leu Pro Ile Ser Ile
                140                 145                 150

Thr Val Phe Leu Phe Ser Val Met Gly Tyr Ser Ile Tyr Arg Tyr
                155                 160                 165
```

117
```

```
Ile His Val Gly Lys Glu Lys His Pro Ala Asn Leu Ile Leu Ile
              170             175             180

Tyr Gly Asn Glu Phe Asp Lys Arg Phe Phe Val Pro Ala Glu Lys
              185             190             195

Ile Val Ile Asn Phe Ile Thr Leu Asn Ile Ser Asp Asp Ser Lys
              200             205             210

Ile Ser His Gln Asp Met Ser Leu Leu Gly Lys Ser Ser Asp Val
              215             220             225

Ser Ser Leu Asn Asp Pro Gln Pro Ser Gly Asn Leu Arg Pro Pro
              230             235             240

Gln Glu Glu Glu Glu Val Lys His Leu Gly Tyr Ala Ser His Leu
              245             250             255

Met Glu Ile Phe Cys Asp Ser Glu Glu Asn Thr Glu Gly Thr Ser
              260             265             270

Leu Thr Gln Gln Glu Ser Leu Ser Arg Thr Ile Pro Pro Asp Lys
              275             280             285

Thr Val Ile Glu Tyr Glu Tyr Asp Val Arg Thr Thr Asp Ile Cys
              290             295             300

Ala Gly Pro Glu Glu Gln Glu Leu Ser Leu Gln Glu Glu Val Ser
              305             310             315

Thr Gln Gly Thr Leu Leu Glu Ser Gln Ala Ala Leu Ala Val Leu
              320             325             330

Gly Pro Gln Thr Leu Gln Tyr Ser Tyr Thr Pro Gln Leu Gln Asp
              335             340             345

Leu Asp Pro Leu Ala Gln Glu His Thr Asp Ser Glu Glu Gly Pro
              350             355             360

Glu Glu Glu Pro Ser Thr Thr Leu Val Asp Trp Asp Pro Gln Thr
              365             370             375

Gly Arg Leu Cys Ile Pro Ser Leu Ser Ser Phe Asp Gln Asp Ser
              380             385             390

Glu Gly Cys Glu Pro Ser Glu Gly Asp Gly Leu Gly Glu Glu Gly
              395             400             405

Leu Leu Ser Arg Leu Tyr Glu Glu Pro Ala Pro Asp Arg Pro Pro
              410             415             420

Gly Glu Asn Glu Thr Tyr Leu Met Gln Phe Met Glu Glu Trp Gly
              425             430             435

Leu Tyr Val Gln Met Glu Asn
              440
```

<210> 105

<211> 21
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-21
<223> Synthetic construct

<400> 105
cgctgctgct gttgctcctg g 21

<210> 106
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 106
cagtgtgcca ggactttg 18

<210> 107
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 107
agtcgcaggc agcgttgg 18

<210> 108
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-25
<223> Synthetic construct.

<400> 108
ctcctccgag tctgtgtgct cctgc 25

<210> 109
<211> 51
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence

<222> 1-51
<223> Synthetic construct.

<400> 109
ggacgggcag ttccctgtgt ctctggtggt ttgcctaaac ctgcaaacat 50

c 51

<210> 110
<211> 1114
<212> DNA
<213> Homo sapiens

<400> 110
cggacgcgtg ggcggacgcg tgggcggacg cgtgggtctc tgcggggaga 50

cgccagcctg cgtctgccat ggggctcggg ttgaggggct ggggacgtcc 100

tctgctgact gtggccaccg ccctgatgct gcccgtgaag cccccccgcag 150

gctcctgggg ggcccagatc atcggggggcc acgaggtgac cccccactcc 200

aggccctaca tggcatccgt gcgcttcggg ggccaacatc actgcggagg 250

cttcctgctg cgagcccgct gggtggtctc ggccgcccac tgcttcagcc 300

acagagacct ccgcactggc ctggtggtgc tgggcgccca cgtcctgagt 350

actgcggagc ccacccagca ggtgtttggc atcgatgctc tcaccacgca 400

ccccgactac caccccatga cccacgccaa cgacatctgc ctgctgcggc 450

tgaacggctc tgctgtcctg ggccctgcag tggggctgct gaggctgcca 500

gggagaaggg ccaggccccc cacagcgggg acacggtgcc gggtggctgg 550

ctggggcttc gtgtctgact ttgaggagct gccgcctgga ctgatggagg 600

ccaaggtccg agtgctggac ccggacgtct gcaacagctc ctggaagggc 650

cacctgacac ttaccatgct ctgcacccgc agtggggaca gccacagacg 700

gggcttctgc tcggccgact ccggagggcc cctggtgtgc aggaaccggg 750

ctcacggcct cgtttccttc tcgggcctct ggtgcggcga ccccaagacc 800

cccgacgtgt acacgcaggt gtccgccttt gtggcctgga tctgggacgt 850

ggttcggcgg agcagtcccc agcccggccc cctgcctggg accaccaggc 900

ccccaggaga agccgcctga gccacaacct tgcggcatgc aaatgagatg 950

gccgctccag gcctggaatg ttccgtggct gggccccacg ggaagcctga 1000

tgttcagggt tggggtggga cgggcagcgg tggggcacac ccattccaca 1050

tgcaaagggc agaagcaaac ccagtaaaat gttaactgac aaaaaaaaaa 1100

120

aaaaaaaaaa gaaa 1114

<210> 111
<211> 283
<212> PRT
<213> Homo sapiens

<400> 111

```
Met Gly Leu Gly Leu Arg Gly Trp Gly Arg Pro Leu Leu Thr Val
 1               5                  10                  15

Ala Thr Ala Leu Met Leu Pro Val Lys Pro Pro Ala Gly Ser Trp
                20                  25                  30

Gly Ala Gln Ile Ile Gly Gly His Glu Val Thr Pro His Ser Arg
                35                  40                  45

Pro Tyr Met Ala Ser Val Arg Phe Gly Gly Gln His His Cys Gly
                50                  55                  60

Gly Phe Leu Leu Arg Ala Arg Trp Val Val Ser Ala Ala His Cys
                65                  70                  75

Phe Ser His Arg Asp Leu Arg Thr Gly Leu Val Val Leu Gly Ala
                80                  85                  90

His Val Leu Ser Thr Ala Glu Pro Thr Gln Gln Val Phe Gly Ile
                95                 100                 105

Asp Ala Leu Thr Thr His Pro Asp Tyr His Pro Met Thr His Ala
               110                 115                 120

Asn Asp Ile Cys Leu Leu Arg Leu Asn Gly Ser Ala Val Leu Gly
               125                 130                 135

Pro Ala Val Gly Leu Leu Arg Leu Pro Gly Arg Arg Ala Arg Pro
               140                 145                 150

Pro Thr Ala Gly Thr Arg Cys Arg Val Ala Gly Trp Gly Phe Val
               155                 160                 165

Ser Asp Phe Glu Glu Leu Pro Pro Gly Leu Met Glu Ala Lys Val
               170                 175                 180

Arg Val Leu Asp Pro Asp Val Cys Asn Ser Ser Trp Lys Gly His
               185                 190                 195

Leu Thr Leu Thr Met Leu Cys Thr Arg Ser Gly Asp Ser His Arg
               200                 205                 210

Arg Gly Phe Cys Ser Ala Asp Ser Gly Gly Pro Leu Val Cys Arg
               215                 220                 225

Asn Arg Ala His Gly Leu Val Ser Phe Ser Gly Leu Trp Cys Gly
               230                 235                 240

Asp Pro Lys Thr Pro Asp Val Tyr Thr Gln Val Ser Ala Phe Val
               245                 250                 255
```

```
Ala Trp Ile Trp Asp Val Val Arg Arg Ser Ser Pro Gln Pro Gly
            260                 265                 270

    Pro Leu Pro Gly Thr Thr Arg Pro Pro Gly Glu Ala Ala
                275                 280
```

<210> 112
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 112
 gacgtctgca acagctcctg gaag 24

<210> 113
<211> 23
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-23
<223> Synthetic construct.

<400> 113
 cgagaaggaa acgaggccgt gag 23

<210> 114
<211> 44
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-44
<223> Synthetic construct.

<400> 114
 tgacacttac catgctctgc acccgcagtg gggacagcca caga 44

<210> 115
<211> 1808
<212> DNA
<213> Homo sapiens

<400> 115
 gagctaccca ggcggctggt gtgcagcaag ctccgcgccg actccggacg 50

 cctgacgcct gacgcctgtc cccggcccgg catgagccgc tacctgctgc 100

 cgctgtcggc gctgggcacg gtagcaggcg ccgccgtgct gctcaaggac 150

 tatgtcaccg gtgggggcttg ccccagcaag gccaccatcc ctgggaagac 200

```
ggtcatcgtg acgggcgcca acacaggcat cgggaagcag accgccttgg 250

aactggccag gagaggaggc aacatcatcc tggcctgccg agacatggag 300

aagtgtgagg cggcagcaaa ggacatccgc ggggagaccc tcaatcacca 350

tgtcaacgcc cggcacctgg acttggcttc cctcaagtct atccgagagt 400

ttgcagcaaa gatcattgaa gaggaggagc gagtggacat tctaatcaac 450

aacgcgggtg tgatgcggtg cccccactgg accaccgagg acggcttcga 500

gatgcagttt ggcgttaacc acctgggtca ctttctcttg acaaacttgc 550

tgctggacaa gctgaaagcc tcagcccctt cgcggatcat caacctctcg 600

tccctggccc atgttgctgg gcacatagac tttgacgact tgaactggca 650

gacgaggaag tataacacca aagccgccta ctgccagagc aagctcgcca 700

tcgtcctctt caccaaggag ctgagccggc ggctgcaagg ctctggtgtg 750

actgtcaacg ccctgcaccc cggcgtggcc aggacagagc tgggcagaca 800

cacgggcatc catggctcca ccttctccag caccacactc gggcccatct 850

tctggctgct ggtcaagagc cccgagctgg ccgcccagcc cagcacatac 900

ctggccgtgg cggaggaact ggcggatgtt tccggaaagt acttcgatgg 950

actcaaacag aaggccccgg cccccgaggc tgaggatgag gaggtggccc 1000

ggaggctttg ggctgaaagt gcccgcctgg tgggcttaga ggctccctct 1050

gtgagggagc agcccctccc cagataacct ctggagcaga tttgaaagcc 1100

aggatggcgc ctccagaccg aggacagctg tccgccatgc ccgcagcttc 1150

ctggcactac ctgagccggg agacccagga ctggcggccg ccatgcccgc 1200

agtaggttct aggggcggt gctggccgca gtggactggc ctgcaggtga 1250

gcactgcccc gggctctggc tggttccgtc tgctctgctg ccagcagggg 1300

agagggccca tctgatgctt cccctgggaa tctaaactgg gaatggccga 1350

ggaggaaggg gctctgtgca cttgcaggcc acgtcaggag agccagcggt 1400

gcctgtcggg gagggttcca aggtgctccg tgaagagcat gggcaagttg 1450

tctgacactt ggtggattct tgggtccctg tgggaccttg tgcatgcatg 1500

gtcctctctg agccttggtt tcttcagcag tgagatgctc agaataactg 1550

ctgtctccca tgatggtgtg gtacagcgag ctgttgtctg gctatggcat 1600

ggctgtgccg ggggtgtttg ctgagggctt cctgtgccag agcccagcca 1650
```

123

```
gagagcaggt gcaggtgtca tcccgagttc aggctctgca cggcatggag 1700

tgggaacccc accagctgct gctacaggac ctgggattgc ctgggactcc 1750

caccttccta tcaattctca tggtagtcca aactgcagac tctcaaactt 1800

gctcattt 1808
```

<210> 116
<211> 331
<212> PRT
<213> Homo sapiens

<400> 116

```
Met Ser Arg Tyr Leu Leu Pro Leu Ser Ala Leu Gly Thr Val Ala
 1               5                  10                  15

Gly Ala Ala Val Leu Leu Lys Asp Tyr Val Thr Gly Gly Ala Cys
                20                  25                  30

Pro Ser Lys Ala Thr Ile Pro Gly Lys Thr Val Ile Val Thr Gly
                35                  40                  45

Ala Asn Thr Gly Ile Gly Lys Gln Thr Ala Leu Glu Leu Ala Arg
                50                  55                  60

Arg Gly Gly Asn Ile Ile Leu Ala Cys Arg Asp Met Glu Lys Cys
                65                  70                  75

Glu Ala Ala Ala Lys Asp Ile Arg Gly Glu Thr Leu Asn His His
                80                  85                  90

Val Asn Ala Arg His Leu Asp Leu Ala Ser Leu Lys Ser Ile Arg
                95                  100                 105

Glu Phe Ala Ala Lys Ile Ile Glu Glu Glu Arg Val Asp Ile
                110                 115                 120

Leu Ile Asn Asn Ala Gly Val Met Arg Cys Pro His Trp Thr Thr
                125                 130                 135

Glu Asp Gly Phe Glu Met Gln Phe Gly Val Asn His Leu Gly His
                140                 145                 150

Phe Leu Leu Thr Asn Leu Leu Leu Asp Lys Leu Lys Ala Ser Ala
                155                 160                 165

Pro Ser Arg Ile Ile Asn Leu Ser Ser Leu Ala His Val Ala Gly
                170                 175                 180

His Ile Asp Phe Asp Asp Leu Asn Trp Gln Thr Arg Lys Tyr Asn
                185                 190                 195

Thr Lys Ala Ala Tyr Cys Gln Ser Lys Leu Ala Ile Val Leu Phe
                200                 205                 210

Thr Lys Glu Leu Ser Arg Arg Leu Gln Gly Ser Gly Val Thr Val
                215                 220                 225
```

124

```
Asn Ala Leu His Pro Gly Val Ala Arg Thr Glu Leu Gly Arg His
            230                 235                 240

Thr Gly Ile His Gly Ser Thr Phe Ser Ser Thr Thr Leu Gly Pro
            245                 250                 255

Ile Phe Trp Leu Leu Val Lys Ser Pro Glu Leu Ala Ala Gln Pro
            260                 265                 270

Ser Thr Tyr Leu Ala Val Ala Glu Glu Leu Ala Asp Val Ser Gly
            275                 280                 285

Lys Tyr Phe Asp Gly Leu Lys Gln Lys Ala Pro Ala Pro Glu Ala
            290                 295                 300

Glu Asp Glu Glu Val Ala Arg Arg Leu Trp Ala Glu Ser Ala Arg
            305                 310                 315

Leu Val Gly Leu Glu Ala Pro Ser Val Arg Glu Gln Pro Leu Pro
            320                 325                 330

Arg
```

<210> 117
<211> 2249
<212> DNA
<213> Homo sapiens

<400> 117

```
gaagttcgcg agcgctggca tgtggtcctg gggcgcggct ggcggcgctg  50

ctggcggtgc tggcgctcgg gacaggagac ccagaaaggg ctgcggctcg 100

gggcgacacg ttctcggcgc tgaccagcgt ggcgcgcgcc ctggcgcccg 150

agcgccggct gctggggctg ctgaggcggt acctgcgcgg ggaggaggcg 200

cggctgcggg acctgactag attctacgac aaggtacttt ctttgcatga 250

ggattcaaca accctgtgg ctaaccctct gcttgcattt actctcatca 300

aacgcctgca gtctgactgg aggaatgtgg tacatagtct ggaggccagt 350

gagaacatcc gagctctgaa ggatggctat gagaaggtgg agcaagacct 400

tccagccttt gaggaccttg agggagcagc aagggccctg atgcggctgc 450

aggacgtgta catgctcaat gtgaaaggcc tggcccgagg tgtctttcag 500

agagtcactg ctctgccat cactgacctg tacagcccca acggctctt 550

ttctctcaca ggggatgact gcttccaagt tggcaaggtg gcctatgaca 600

tgggggatta ttaccatgcc attccatggc tggaggaggc tgtcagtctc 650

ttccgaggat cttacggaga gtggaagaca gaggatgagg caagtctaga 700
```

125

agatgccttg gatcacttgg cctttgctta tttccgggca ggaaatgttt 750

cgtgtgccct cagcctctct cgggagtttc ttctctacag cccagataat 800

aagaggatgg ccaggaatgt cttgaaatat gaaaggctct tggcagagag 850

ccccaaccac gtggtagctg aggctgtcat ccagaggccc aatataccccc 900

acctgcagac cagagacacc tacgagggggc tatgtcagac cctgggttcc 950

cagcccactc tctaccagat ccctagcctc tactgttcct atgagaccaa 1000

ttccaacgcc tacctgctgc tccagcccat ccggaaggag gtcatccacc 1050

tggagcccta cattgctctc taccatgact tcgtcagtga ctcagaggct 1100

cagaaaatta gagaacttgc agaaccatgg ctacagaggt cagtggtggc 1150

atcaggggag aagcagttac aagtggagta ccgcatcagc aaaagtgcct 1200

ggctgaagga cactgttgac ccaaaactgg tgaccctcaa ccaccgcatt 1250

gctgccctca caggccttga tgtccggcct ccctatgcag agtatctgca 1300

ggtggtgaac tatggcatcg gaggacacta tgagcctcac tttgaccatg 1350

ctacgtcacc aagcagcccc ctctacagaa tgaagtcagg aaaccgagtt 1400

gcaacattta tgatctatct gagctcggtg gaagctggag gagccacagc 1450

cttcatctat gccaacctca gcgtgcctgt ggttaggaat gcagcactgt 1500

tttggtggaa cctgcacagg agtggtgaag gggacagtga cacacttcat 1550

gctggctgtc ctgtcctggt gggagataag tgggtggcca acaagtggat 1600

acatgagtat ggacaggaat tccgcagacc ctgcagctcc agccctgaag 1650

actgaactgt tggcagagag aagctggtgg agtcctgtgg ctttccagag 1700

aagccaggag ccaaaagctg gggtaggaga ggagaaagca gagcagcctc 1750

ctggaagaag gccttgtcag ctttgtctgt gcctcgcaaa tcagaggcaa 1800

gggagaggtt gttaccaggg gacactgaga atgtacattt gatctgcccc 1850

agccacggaa gtcagagtag gatgcacagt acaaaggagg ggggagtgga 1900

ggcctgagag ggaagtttct ggagttcaga tactctctgt tgggaacagg 1950

acatctcaac agtctcaggt tcgatcagtg ggtctttttgg cactttgaac 2000

cttgaccaca gggaccaaga agtggcaatg aggacacctg caggaggggc 2050

tagcctgact cccagaactt taagactttc tccccactgc cttctgctgc 2100

agcccaagca gggagtgtcc ccctcccaga agcatatccc agatgagtgg 2150

126

tacattatat aaggattttt tttaagttga aaacaacttt cttttctttt 2200

tgtatgatgg tttttaaca cagtcattaa aaatgtttat aaatcaaaa 2249

<210> 118
<211> 544
<212> PRT
<213> Homo sapiens

<400> 118
Met Gly Pro Gly Ala Arg Leu Ala Ala Leu Leu Ala Val Leu Ala
1   5   10   15

Leu Gly Thr Gly Asp Pro Glu Arg Ala Ala Ala Arg Gly Asp Thr
                20   25   30

Phe Ser Ala Leu Thr Ser Val Ala Arg Ala Leu Ala Pro Glu Arg
                35   40   45

Arg Leu Leu Gly Leu Leu Arg Arg Tyr Leu Arg Gly Glu Glu Ala
                50   55   60

Arg Leu Arg Asp Leu Thr Arg Phe Tyr Asp Lys Val Leu Ser Leu
                65   70   75

His Glu Asp Ser Thr Thr Pro Val Ala Asn Pro Leu Leu Ala Phe
                80   85   90

Thr Leu Ile Lys Arg Leu Gln Ser Asp Trp Arg Asn Val Val His
                95   100   105

Ser Leu Glu Ala Ser Glu Asn Ile Arg Ala Leu Lys Asp Gly Tyr
                110   115   120

Glu Lys Val Glu Gln Asp Leu Pro Ala Phe Glu Asp Leu Glu Gly
                125   130   135

Ala Ala Arg Ala Leu Met Arg Leu Gln Asp Val Tyr Met Leu Asn
                140   145   150

Val Lys Gly Leu Ala Arg Gly Val Phe Gln Arg Val Thr Gly Ser
                155   160   165

Ala Ile Thr Asp Leu Tyr Ser Pro Lys Arg Leu Phe Ser Leu Thr
                170   175   180

Gly Asp Asp Cys Phe Gln Val Gly Lys Val Ala Tyr Asp Met Gly
                185   190   195

Asp Tyr Tyr His Ala Ile Pro Trp Leu Glu Glu Ala Val Ser Leu
                200   205   210

Phe Arg Gly Ser Tyr Gly Glu Trp Lys Thr Glu Asp Glu Ala Ser
                215   220   225

Leu Glu Asp Ala Leu Asp His Leu Ala Phe Ala Tyr Phe Arg Ala
                230   235   240

127

```
Gly Asn Val Ser Cys Ala Leu Ser Leu Ser Arg Glu Phe Leu Leu
                245             250                 255

Tyr Ser Pro Asp Asn Lys Arg Met Ala Arg Asn Val Leu Lys Tyr
                260             265                 270

Glu Arg Leu Leu Ala Glu Ser Pro Asn His Val Val Ala Glu Ala
                275             280                 285

Val Ile Gln Arg Pro Asn Ile Pro His Leu Gln Thr Arg Asp Thr
                290             295                 300

Tyr Glu Gly Leu Cys Gln Thr Leu Gly Ser Gln Pro Thr Leu Tyr
                305             310                 315

Gln Ile Pro Ser Leu Tyr Cys Ser Tyr Glu Thr Asn Ser Asn Ala
                320             325                 330

Tyr Leu Leu Leu Gln Pro Ile Arg Lys Glu Val Ile His Leu Glu
                335             340                 345

Pro Tyr Ile Ala Leu Tyr His Asp Phe Val Ser Asp Ser Glu Ala
                350             355                 360

Gln Lys Ile Arg Glu Leu Ala Glu Pro Trp Leu Gln Arg Ser Val
                365             370                 375

Val Ala Ser Gly Glu Lys Gln Leu Gln Val Glu Tyr Arg Ile Ser
                380             385                 390

Lys Ser Ala Trp Leu Lys Asp Thr Val Asp Pro Lys Leu Val Thr
                395             400                 405

Leu Asn His Arg Ile Ala Ala Leu Thr Gly Leu Asp Val Arg Pro
                410             415                 420

Pro Tyr Ala Glu Tyr Leu Gln Val Val Asn Tyr Gly Ile Gly Gly
                425             430                 435

His Tyr Glu Pro His Phe Asp His Ala Thr Ser Pro Ser Ser Pro
                440             445                 450

Leu Tyr Arg Met Lys Ser Gly Asn Arg Val Ala Thr Phe Met Ile
                455             460                 465

Tyr Leu Ser Ser Val Glu Ala Gly Gly Ala Thr Ala Phe Ile Tyr
                470             475                 480

Ala Asn Leu Ser Val Pro Val Val Arg Asn Ala Ala Leu Phe Trp
                485             490                 495

Trp Asn Leu His Arg Ser Gly Glu Gly Asp Ser Asp Thr Leu His
                500             505                 510

Ala Gly Cys Pro Val Leu Val Gly Asp Lys Trp Val Ala Asn Lys
                515             520                 525

Trp Ile His Glu Tyr Gly Gln Glu Phe Arg Arg Pro Cys Ser Ser
```

128

Ser Pro Glu Asp

<210> 119
<211> 23
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-23
<223> Synthetic construct.

<400> 119
 cgggacagga gacccagaaa ggg 23

<210> 120
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 120
 ggccaagtga tccaaggcat cttc 24

<210> 121
<211> 49
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-49
<223> Synthetic construct.

<400> 121
 ctgcgggacc tgactagatt ctacgacaag gtactttctt tgcatgggg 49

<210> 122
<211> 1778
<212> DNA
<213> Homo sapiens

<400> 122
 gagataggga gtctgggttt aagttcctgc tccatctcag gagcccctgc 50

 tcccacccct aggaagccac cagactccac ggtgtggggc caatcaggtg 100

 gaatcggccc tggcaggtgg ggccacgagc gctggctgag ggaccgagcc 150

 ggagagcccc ggagcccccg taacccgcgc ggggagcgcc caggatgccg 200

cgcggggact cggagcaggt gcgctactgc gcgcgcttct cctacctctg 250

gctcaagttt tcacttatca tctattccac cgtgttctgg ctgattgggg 300

ccctggtcct gtctgtgggc atctatgcag aggttgagcg gcagaaatat 350

aaaacccttg aaagtgcctt cctggctcca gccatcatcc tcatcctcct 400

gggcgtcgtc atgttcatgg tctccttcat tggtgtgctg gcgtccctcc 450

gtgacaacct gtaccttctc caagcattca tgtacatcct tgggatctgc 500

ctcatcatgg agctcattgg tggcgtggtg gccttgacct tccggaacca 550

gaccattgac ttcctgaacg acaacattcg aagaggaatt gagaactact 600

atgatgatct ggacttcaaa aacatcatgg actttgttca gaaaaagttc 650

aagtgctgtg gcggggagga ctaccgagat tggagcaaga atcagtacca 700

cgactgcagt gcccctggac ccctggcctg tggggtgccc tacacctgct 750

gcatcaggaa cacgacagaa gttgtcaaca ccatgtgtgg ctacaaaact 800

atcgacaagg agcgtttcag tgtgcaggat gtcatctacg tgcggggctg 850

caccaacgcc gtgatcatct ggttcatgga caactacacc atcatggcgt 900

gcatcctcct gggcatcctg cttccccagt tcctgggggt gctgctgacg 950

ctgctgtaca tcacccgggt ggaggacatc atcatggagc actctgtcac 1000

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cgggatgctg cttgtgctac cccaattagg gcccagcctg ccatggcagc 1100

tccaacaagg accgtctggg atagcacctc tcagtcaaca tcgtggggct 1150

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gctgtgtgtg cctgtgtgta ggtcccacgg cctctgcctc cccaggagc 1250

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gtgcccacct ggggcctggg gaacaaggcc ctcctttctc caggcctggg 1350

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gggcaggagg gaagagctgt ccatgcagcc acgcccatgg ccaggttggc 1550

ctcttctcag cctcccaggt gccttgagcc ctcttgcaag ggcggctgct 1600

tccttgagcc tagttttttt ttacgtgatt tttgtaacat tcattttttt 1650

130

gtacagataa caggagtttc tgactaatca aagctggtat ttccccgcat 1700

gtcttattct tgcccttccc ccaaccagtt tgttaatcaa acaataaaaa 1750

catgttttgt tttgttttta aaaaaaaa 1778

<210> 123
<211> 294
<212> PRT
<213> Homo sapiens

<400> 123

Met	Pro	Arg	Gly	Asp	Ser	Glu	Gln	Val	Arg	Tyr	Cys	Ala	Arg	Phe
1				5					10					15

Ser	Tyr	Leu	Trp	Leu	Lys	Phe	Ser	Leu	Ile	Ile	Tyr	Ser	Thr	Val
			20					25						30

Phe	Trp	Leu	Ile	Gly	Ala	Leu	Val	Leu	Ser	Val	Gly	Ile	Tyr	Ala
				35					40					45

Glu	Val	Glu	Arg	Gln	Lys	Tyr	Lys	Thr	Leu	Glu	Ser	Ala	Phe	Leu
				50					55					60

Ala	Pro	Ala	Ile	Ile	Leu	Ile	Leu	Leu	Gly	Val	Val	Met	Phe	Met
				65					70					75

Val	Ser	Phe	Ile	Gly	Val	Leu	Ala	Ser	Leu	Arg	Asp	Asn	Leu	Tyr
				80					85					90

Leu	Leu	Gln	Ala	Phe	Met	Tyr	Ile	Leu	Gly	Ile	Cys	Leu	Ile	Met
				95					100					105

Glu	Leu	Ile	Gly	Gly	Val	Val	Ala	Leu	Thr	Phe	Arg	Asn	Gln	Thr
				110					115					120

Ile	Asp	Phe	Leu	Asn	Asp	Asn	Ile	Arg	Arg	Gly	Ile	Glu	Asn	Tyr
				125					130					135

Tyr	Asp	Asp	Leu	Asp	Phe	Lys	Asn	Ile	Met	Asp	Phe	Val	Gln	Lys
				140					145					150

Lys	Phe	Lys	Cys	Cys	Gly	Gly	Glu	Asp	Tyr	Arg	Asp	Trp	Ser	Lys
				155					160					165

Asn	Gln	Tyr	His	Asp	Cys	Ser	Ala	Pro	Gly	Pro	Leu	Ala	Cys	Gly
				170					175					180

Val	Pro	Tyr	Thr	Cys	Cys	Ile	Arg	Asn	Thr	Thr	Glu	Val	Val	Asn
				185					190					195

Thr	Met	Cys	Gly	Tyr	Lys	Thr	Ile	Asp	Lys	Glu	Arg	Phe	Ser	Val
				200					205					210

Gln	Asp	Val	Ile	Tyr	Val	Arg	Gly	Cys	Thr	Asn	Ala	Val	Ile	Ile
				215					220					225

Trp	Phe	Met	Asp	Asn	Tyr	Thr	Ile	Met	Ala	Cys	Ile	Leu	Leu	Gly

131

Ile Leu Leu Pro Gln Phe Leu Gly Val Leu Leu Thr Leu Leu Tyr
                245   250   255

Ile Thr Arg Val Glu Asp Ile Ile Met Glu His Ser Val Thr Asp
                260   265   270

Gly Leu Leu Gly Pro Gly Ala Lys Pro Ser Val Glu Ala Ala Gly
                275   280   285

Thr Gly Cys Cys Leu Cys Tyr Pro Asn
                290

<210> 124
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-25
<223> Synthetic construct.

<400> 124
 atcatctatt ccaccgtgtt ctggc 25

<210> 125
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-25
<223> Synthetic construct.

<400> 125
 gacagagtgc tccatgatga tgtcc 25

<210> 126
<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 126
 cctgtctgtg ggcatctatg cagaggttga gcggcagaaa tataaaaccc 50

<210> 127
<211> 1636
<212> DNA
<213> Homo sapiens

<400> 127

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gaggagcggg  ccgaggactc  cagcgtgccc  aggtctggca  tcctgcactt  50

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ctctgtggtt  tgctggcagc  caccttgatc  caagccaccc  tcagtcccac  150

tgcagttctc  atcctcggcc  caaaagtcat  caaagaaaag  ctgacacagg  200

agctgaagga  ccacaacgcc  accagcatcc  tgcagcagct  gccgctgctc  250

agtgccatgc  gggaaaagcc  agccggaggc  atccctgtgc  tgggcagcct  300

ggtgaacacc  gtcctgaagc  acatcatctg  gctgaaggtc  atcacagcta  350

acatcctcca  gctgcaggtg  aagccctcgg  ccaatgacca  ggagctgcta  400

gtcaagatcc  ccctggacat  ggtggctgga  ttcaacacgc  ccctggtcaa  450

gaccatcgtg  gagttccaca  tgacgactga  ggcccaagcc  accatccgca  500

tggacaccag  tgcaagtggc  cccacccgcc  tggtcctcag  tgactgtgcc  550

accagccatg  ggagcctgcg  catccaactg  ctgtataagc  tctccttcct  600

ggtgaacgcc  ttagctaagc  aggtcatgaa  cctcctagtg  ccatccctgc  650

ccaatctagt  gaaaaaccag  ctgtgtcccg  tgatcgaggc  ttccttcaat  700

ggcatgtatg  cagacctcct  gcagctggtg  aaggtgccca  tttccctcag  750

cattgaccgt  ctggagtttg  accttctgta  tcctgccatc  aagggtgaca  800

ccattcagct  ctacctgggg  gccaagttgt  tggactcaca  gggaaaggtg  850

accaagtggt  tcaataactc  tgcagcttcc  ctgacaatgc  ccaccctgga  900

caacatcccg  ttcagcctca  tcgtgagtca  ggacgtggtg  aaagctgcag  950

tggctgctgt  gctctctcca  gaagaattca  tggtcctgtt  ggactctgtg  1000

cttcctgaga  gtgcccatcg  gctgaagtca  agcatcgggc  tgatcaatga  1050

aaaggctgca  gataagctgg  gatctaccca  gatcgtgaag  atcctaactc  1100

aggacactcc  cgagtttttt  atagaccaag  gccatgccaa  ggtggcccaa  1150

ctgatcgtgc  tggaagtgtt  tccctccagt  gaagccctcc  gccctttgtt  1200

caccctgggc  atcgaagcca  gctcggaagc  tcagttttac  accaaaggtg  1250

accaacttat  actcaacttg  aataacatca  gctctgatcg  gatccagctg  1300

atgaactctg  ggattggctg  gttccaacct  gatgttctga  aaaacatcat  1350

cactgagatc  atccactcca  tcctgctgcc  gaaccagaat  ggcaaattaa  1400

gatctggggt  cccagtgtca  ttggtgaagg  ccttgggatt  cgaggcagct  1450
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133

gagtcctcac tgaccaagga tgcccttgtg cttactccag cctccttgtg 1500

gaaacccagc tctcctgtct cccagtgaag acttggatgg cagccatcag 1550

ggaaggctgg gtcccagctg ggagtatggg tgtgagctct atagaccatc 1600

cctctctgca atcaataaac acttgcctgt gaaaaa 1636

<210> 128
<211> 484
<212> PRT
<213> Homo sapiens

<400> 128

```
Met Ala Gly Pro Trp Thr Phe Thr Leu Leu Cys Gly Leu Leu Ala
1               5                   10                  15

Ala Thr Leu Ile Gln Ala Thr Leu Ser Pro Thr Ala Val Leu Ile
                20                  25                  30

Leu Gly Pro Lys Val Ile Lys Glu Lys Leu Thr Gln Glu Leu Lys
                35                  40                  45

Asp His Asn Ala Thr Ser Ile Leu Gln Gln Leu Pro Leu Leu Ser
                50                  55                  60

Ala Met Arg Glu Lys Pro Ala Gly Gly Ile Pro Val Leu Gly Ser
                65                  70                  75

Leu Val Asn Thr Val Leu Lys His Ile Ile Trp Leu Lys Val Ile
                80                  85                  90

Thr Ala Asn Ile Leu Gln Leu Gln Val Lys Pro Ser Ala Asn Asp
                95                  100                 105

Gln Glu Leu Leu Val Lys Ile Pro Leu Asp Met Val Ala Gly Phe
                110                 115                 120

Asn Thr Pro Leu Val Lys Thr Ile Val Glu Phe His Met Thr Thr
                125                 130                 135

Glu Ala Gln Ala Thr Ile Arg Met Asp Thr Ser Ala Ser Gly Pro
                140                 145                 150

Thr Arg Leu Val Leu Ser Asp Cys Ala Thr Ser His Gly Ser Leu
                155                 160                 165

Arg Ile Gln Leu Leu Tyr Lys Leu Ser Phe Leu Val Asn Ala Leu
                170                 175                 180

Ala Lys Gln Val Met Asn Leu Leu Val Pro Ser Leu Pro Asn Leu
                185                 190                 195

Val Lys Asn Gln Leu Cys Pro Val Ile Glu Ala Ser Phe Asn Gly
                200                 205                 210

Met Tyr Ala Asp Leu Leu Gln Leu Val Lys Val Pro Ile Ser Leu
                215                 220                 225
```

134

```
Ser Ile Asp Arg Leu Glu Phe Asp Leu Leu Tyr Pro Ala Ile Lys
            230                 235                     240

Gly Asp Thr Ile Gln Leu Tyr Leu Gly Ala Lys Leu Leu Asp Ser
            245                 250                     255

Gln Gly Lys Val Thr Lys Trp Phe Asn Asn Ser Ala Ala Ser Leu
            260                 265                     270

Thr Met Pro Thr Leu Asp Asn Ile Pro Phe Ser Leu Ile Val Ser
            275                 280                     285

Gln Asp Val Val Lys Ala Ala Val Ala Ala Val Leu Ser Pro Glu
            290                 295                     300

Glu Phe Met Val Leu Leu Asp Ser Val Leu Pro Glu Ser Ala His
            305                 310                     315

Arg Leu Lys Ser Ser Ile Gly Leu Ile Asn Glu Lys Ala Ala Asp
            320                 325                     330

Lys Leu Gly Ser Thr Gln Ile Val Lys Ile Leu Thr Gln Asp Thr
            335                 340                     345

Pro Glu Phe Phe Ile Asp Gln Gly His Ala Lys Val Ala Gln Leu
            350                 355                     360

Ile Val Leu Glu Val Phe Pro Ser Ser Glu Ala Leu Arg Pro Leu
            365                 370                     375

Phe Thr Leu Gly Ile Glu Ala Ser Ser Glu Ala Gln Phe Tyr Thr
            380                 385                     390

Lys Gly Asp Gln Leu Ile Leu Asn Leu Asn Asn Ile Ser Ser Asp
            395                 400                     405

Arg Ile Gln Leu Met Asn Ser Gly Ile Gly Trp Phe Gln Pro Asp
            410                 415                     420

Val Leu Lys Asn Ile Ile Thr Glu Ile Ile His Ser Ile Leu Leu
            425                 430                     435

Pro Asn Gln Asn Gly Lys Leu Arg Ser Gly Val Pro Val Ser Leu
            440                 445                     450

Val Lys Ala Leu Gly Phe Glu Ala Ala Glu Ser Ser Leu Thr Lys
            455                 460                     465

Asp Ala Leu Val Leu Thr Pro Ala Ser Leu Trp Lys Pro Ser Ser
            470                 475                     480

Pro Val Ser Gln


<210> 129
<211> 2213
<212> DNA
<213> Homo sapiens


135
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<400> 129

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gtggtggcgc tgctcatcgt ttgcgacgtt ccctcagcct ctgcccaaag 100

aaagaaggag atggtgttat ctgaaaaggt tagtcagctg atggaatgga 150

ctaacaaaag acctgtaata agaatgaatg gagacaagtt ccgtcgcctt 200

gtgaaagccc caccgagaaa ttactccgtt atcgtcatgt tcactgctct 250

ccaactgcat agacagtgtg tcgtttgcaa gcaagctgat gaagaattcc 300

agatcctggc aaactcctgg cgatactcca gtgcattcac caacaggata 350

tttttttgcca tggtggattt tgatgaaggc tctgatgtat ttcagatgct 400

aaacatgaat tcagctccaa ctttcatcaa ctttcctgca aaagggaaac 450

ccaaacgggg tgatacatat gagttacagg tgcggggttt ttcagctgag 500

cagattgccc ggtggatcgc cgacagaact gatgtcaata ttagagtgat 550

tagacccccca aattatgctg gtccccttat gttgggattg cttttggctg 600

ttattggtgg acttgtgtat cttcgaagaa gtaatatgga atttctcttt 650

aataaaactg gatgggcttt tgcagctttg tgttttgtgc ttgctatgac 700

atctggtcaa atgtggaacc atataagagg accaccatat gcccataaga 750

atccccacac gggacatgtg aattatatcc atggaagcag tcaagcccag 800

tttgtagctg aaacacacat tgttcttctg tttaatggtg gagttacctt 850

aggaatggtg cttttatgtg aagctgctac ctctgacatg gatattggaa 900

agcgaaagat aatgtgtgtg ctggtattg gacttgttgt attattcttc 950

agttggatgc tctctatttt tagatctaaa tatcatggct acccatacag 1000

ctttctgatg agttaaaaag gtcccagaga tatatagaca ctggagtact 1050

ggaaattgaa aaacgaaaat cgtgtgtgtt tgaaaagaag aatgcaactt 1100

gtatattttg tattacctct ttttttcaag tgatttaaat agttaatcat 1150

ttaaccaaag aagatgtgta gtgccttaac aagcaatcct ctgtcaaaat 1200

ctgaggtatt tgaaaataat tatcctctta accttctctt cccagtgaac 1250

tttatggaac atttaattta gtacaattaa gtatattata aaaattgtaa 1300

aactactact ttgtttagt tagaacaaag ctcaaaacta ctttagttaa 1350

cttggtcatc tgattttata ttgccttatc caaagatggg gaaagtaagt 1400

cctgaccagg tgttcccaca tatgcctgtt acagataact acattaggaa 1450
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136

ttcattctta gcttcttcat ctttgtgtgg atgtgtatac tttacgcatc 1500

tttccttttg agtagagaaa ttatgtgtgt catgtggtct tctgaaaatg 1550

gaacaccatt cttcagagca cacgtctagc cctcagcaag acagttgttt 1600

ctcctcctcc ttgcatattt cctactgcgc tccagcctga gtgatagagt 1650

gagactctgt ctcaaaaaaa agtatctcta aatacaggat tataatttct 1700

gcttgagtat ggtgttaact accttgtatt tagaaagatt tcagattcat 1750

tccatctcct tagttttctt ttaaggtgac ccatctgtga taaaaatata 1800

gcttagtgct aaaatcagtg taacttatac atggcctaaa atgtttctac 1850

aaattagagt ttgtcactta ttccatttgt acctaagaga aaaataggct 1900

cagttagaaa aggactccct ggccaggcgc agtgacttac gcctgtaatc 1950

tcagcacttt gggaggccaa ggcaggcaga tcacgaggtc aggagttcga 2000

gaccatcctg gccaacatgg tgaaaccccg tctctactaa aaatataaaa 2050

attagctggg tgtggtggca ggagcctgta atcccagcta cacaggaggc 2100

tgaggcacga gaatcacttg aactcaggag atggaggttt cagtgagccg 2150

agatcacgcc actgcactcc agcctggcaa cagagcgaga ctccatctca 2200

aaaaaaaaaa aaa 2213

<210> 130
<211> 335
<212> PRT
<213> Homo sapiens

<400> 130
Met Ala Ala Arg Trp Arg Phe Trp Cys Val Ser Val Thr Met Val
 1   5   10   15

Val Ala Leu Leu Ile Val Cys Asp Val Pro Ser Ala Ser Ala Gln
                20   25   30

Arg Lys Lys Glu Met Val Leu Ser Glu Lys Val Ser Gln Leu Met
                35   40   45

Glu Trp Thr Asn Lys Arg Pro Val Ile Arg Met Asn Gly Asp Lys
                50   55   60

Phe Arg Arg Leu Val Lys Ala Pro Pro Arg Asn Tyr Ser Val Ile
                65   70   75

Val Met Phe Thr Ala Leu Gln Leu His Arg Gln Cys Val Val Cys
                80   85   90

Lys Gln Ala Asp Glu Glu Phe Gln Ile Leu Ala Asn Ser Trp Arg
                95   100   105

137

```
Tyr Ser Ser Ala Phe Thr Asn Arg Ile Phe Phe Ala Met Val Asp
            110               115               120

Phe Asp Glu Gly Ser Asp Val Phe Gln Met Leu Asn Met Asn Ser
            125               130               135

Ala Pro Thr Phe Ile Asn Phe Pro Ala Lys Gly Lys Pro Lys Arg
            140               145               150

Gly Asp Thr Tyr Glu Leu Gln Val Arg Gly Phe Ser Ala Glu Gln
            155               160               165

Ile Ala Arg Trp Ile Ala Asp Arg Thr Asp Val Asn Ile Arg Val
            170               175               180

Ile Arg Pro Pro Asn Tyr Ala Gly Pro Leu Met Leu Gly Leu Leu
            185               190               195

Leu Ala Val Ile Gly Gly Leu Val Tyr Leu Arg Arg Ser Asn Met
            200               205               210

Glu Phe Leu Phe Asn Lys Thr Gly Trp Ala Phe Ala Ala Leu Cys
            215               220               225

Phe Val Leu Ala Met Thr Ser Gly Gln Met Trp Asn His Ile Arg
            230               235               240

Gly Pro Pro Tyr Ala His Lys Asn Pro His Thr Gly His Val Asn
            245               250               255

Tyr Ile His Gly Ser Ser Gln Ala Gln Phe Val Ala Glu Thr His
            260               265               270

Ile Val Leu Leu Phe Asn Gly Gly Val Thr Leu Gly Met Val Leu
            275               280               285

Leu Cys Glu Ala Ala Thr Ser Asp Met Asp Ile Gly Lys Arg Lys
            290               295               300

Ile Met Cys Val Ala Gly Ile Gly Leu Val Val Leu Phe Phe Ser
            305               310               315

Trp Met Leu Ser Ile Phe Arg Ser Lys Tyr His Gly Tyr Pro Tyr
            320               325               330

Ser Phe Leu Met Ser
            335
```

<210> 131
<211> 2476
<212> DNA
<213> Homo sapiens

<400> 131
 aagcaaccaa actgcaagct ttgggagttg ttcgctgtcc ctgccctgct 50

 ctgctaggga gagaacgcca gagggaggcg gctggcccgg cggcaggctc 100

```
tcagaaccgc taccggcgat gctactgctg tgggtgtcgg tggtcgcagc 150

cttggcgctg gcggtactgg cccccggagc aggggagcag aggcggagag 200

cagccaaagc gcccaatgtg gtgctggtcg tgagcgactc cttcgatgga 250

aggttaacat ttcatccagg aagtcaggta gtgaaacttc cttttatcaa 300

ctttatgaag acacgtggga cttcctttct gaatgcctac acaaactctc 350

caatttgttg cccatcacgc gcagcaatgt ggagtggcct cttcactcac 400

ttaacagaat cttggaataa ttttaagggt ctagatccaa attatacaac 450

atggatggat gtcatggaga ggcatggcta ccgaacacag aaatttggga 500

aactggacta tacttcagga catcactcca ttagtaatcg tgtggaagcg 550

tggacaagag atgttgcttt cttactcaga caagaaggca ggcccatggt 600

taatcttatc cgtaacagga ctaaagtcag agtgatggaa agggattggc 650

agaatacaga caaagcagta aactggttaa gaaaggaagc aattaattac 700

actgaaccat ttgttattta cttgggatta aatttaccac acccttaccc 750

ttcaccatct tctggagaaa attttggatc ttcaacattt cacacatctc 800

tttattggct tgaaaaagtg tctcatgatg ccatcaaaat cccaaagtgg 850

tcacctttgt cagaaatgca ccctgtagat tattactctt cttatacaaa 900

aaactgcact ggaagattta caaaaaaaga aattaagaat attagagcat 950

tttattatgc tatgtgtgct gagacagatg ccatgcttgg tgaaattatt 1000

ttggcccttc atcaattaga tcttcttcag aaaactattg tcatatactc 1050

ctcagaccat ggagagctgg ccatggaaca tcgacagttt tataaaatga 1100

gcatgtacga ggctagtgca catgttccgc ttttgatgat gggaccagga 1150

attaaagccg gcctacaagt atcaaatgtg gtttctcttg tggatattta 1200

ccctaccatg cttgatattg ctggaattcc tctgcctcag aacctgagtg 1250

gatactcttt gttgccgtta tcatcagaaa catttaagaa tgaacataaa 1300

gtcaaaaacc tgcatccacc ctggattctg agtgaattcc atggatgtaa 1350

tgtgaatgcc tccacctaca tgcttcgaac taaccactgg aaatatatag 1400

cctattcgga tggtgcatca atattgcctc aactctttga tctttcctcg 1450

gatccagatg aattaacaaa tgttgctgta aaatttccag aaattactta 1500

ttctttggat cagaagcttc attccattat aaactaccct aaagtttctg 1550
```

139

```
cttctgtcca ccagtataat aaagagcagt ttatcaagtg gaaacaaagt 1600

ataggacaga attattcaaa cgttatagca aatcttaggt ggcaccaaga 1650

ctggcagaag gaaccaagga agtatgaaaa tgcaattgat cagtggctta 1700

aaacccatat gaatccaaga gcagtttgaa caaaaagttt aaaaatagtg 1750

ttctagagat acatataaat atattacaag atcataatta tgtattttaa 1800

atgaaacagt tttaataatt accaagtttt ggccgggcac agtggctcac 1850

acctgtaatc ccaggacttt gggaggctga ggaaagcaga tcacaaggtc 1900

aagagattga gaccatcctg gccaacatgg tgaaaccctg tctctactaa 1950

aaatacaaaa attagctggg cgcggtggtg cacacctata gtctcagcta 2000

ctcagaggct gaggcaggag gatcgcttga acccgggagg cagcagttgc 2050

agtgagctga gattgcgcca ctgtactcca gcctggcaac agagtgagac 2100

tgtgtcgcaa aaaataaaa ataaataat aataattacc aattttttcat 2150

tattttgtaa gaatgtagtg tattttaaga taaaatgcca atgattataa 2200

aatcacatat tttcaaaaat ggttattatt taggcctttg tacaatttct 2250

aacaatttag tggaagtatc aaaaggattg aagcaaatac tgtaacagtt 2300

atgttccttt aaataataga gaatataaaa tattgtaata atatgtatca 2350

taaaatagtt gtatgtgagc atttgatggt gaaaaaaaaa aaaaaaaaaa 2400

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2450

aaaaaaaaaa aaaaaaaaaa aaaaaa 2476
```
<210> 132
<211> 536
<212> PRT
<213> Homo sapiens

<400> 132
```
    Met Leu Leu Leu Trp Val Ser Val Val Ala Ala Leu Ala Leu Ala
    1               5                   10                  15

    Val Leu Ala Pro Gly Ala Gly Glu Gln Arg Arg Ala Ala Lys
                    20                  25                  30

    Ala Pro Asn Val Val Leu Val Val Ser Asp Ser Phe Asp Gly Arg
                    35                  40                  45

    Leu Thr Phe His Pro Gly Ser Gln Val Val Lys Leu Pro Phe Ile
                    50                  55                  60

    Asn Phe Met Lys Thr Arg Gly Thr Ser Phe Leu Asn Ala Tyr Thr
                    65                  70                  75
```

140

Asn Ser Pro Ile Cys Cys Pro Ser Arg Ala Ala Met Trp Ser Gly
                    80   85   90

Leu Phe Thr His Leu Thr Glu Ser Trp Asn Asn Phe Lys Gly Leu
                    95   100   105

Asp Pro Asn Tyr Thr Thr Trp Met Asp Val Met Glu Arg His Gly
                    110   115   120

Tyr Arg Thr Gln Lys Phe Gly Lys Leu Asp Tyr Thr Ser Gly His
                    125   130   135

His Ser Ile Ser Asn Arg Val Glu Ala Trp Thr Arg Asp Val Ala
                    140   145   150

Phe Leu Leu Arg Gln Glu Gly Arg Pro Met Val Asn Leu Ile Arg
                    155   160   165

Asn Arg Thr Lys Val Arg Val Met Glu Arg Asp Trp Gln Asn Thr
                    170   175   180

Asp Lys Ala Val Asn Trp Leu Arg Lys Glu Ala Ile Asn Tyr Thr
                    185   190   195

Glu Pro Phe Val Ile Tyr Leu Gly Leu Asn Leu Pro His Pro Tyr
                    200   205   210

Pro Ser Pro Ser Ser Gly Glu Asn Phe Gly Ser Ser Thr Phe His
                    215   220   225

Thr Ser Leu Tyr Trp Leu Glu Lys Val Ser His Asp Ala Ile Lys
                    230   235   240

Ile Pro Lys Trp Ser Pro Leu Ser Glu Met His Pro Val Asp Tyr
                    245   250   255

Tyr Ser Ser Tyr Thr Lys Asn Cys Thr Gly Arg Phe Thr Lys Lys
                    260   265   270

Glu Ile Lys Asn Ile Arg Ala Phe Tyr Tyr Ala Met Cys Ala Glu
                    275   280   285

Thr Asp Ala Met Leu Gly Glu Ile Ile Leu Ala Leu His Gln Leu
                    290   295   300

Asp Leu Leu Gln Lys Thr Ile Val Ile Tyr Ser Ser Asp His Gly
                    305   310   315

Glu Leu Ala Met Glu His Arg Gln Phe Tyr Lys Met Ser Met Tyr
                    320   325   330

Glu Ala Ser Ala His Val Pro Leu Leu Met Met Gly Pro Gly Ile
                    335   340   345

Lys Ala Gly Leu Gln Val Ser Asn Val Val Ser Leu Val Asp Ile
                    350   355   360

Tyr Pro Thr Met Leu Asp Ile Ala Gly Ile Pro Leu Pro Gln Asn

141

```
Leu Ser Gly Tyr Ser Leu Leu Pro Leu Ser Ser Glu Thr Phe Lys
            380                 385                 390
```

```
Asn Glu His Lys Val Lys Asn Leu His Pro Pro Trp Ile Leu Ser
            395                 400                 405
```

```
Glu Phe His Gly Cys Asn Val Asn Ala Ser Thr Tyr Met Leu Arg
            410                 415                 420
```

```
Thr Asn His Trp Lys Tyr Ile Ala Tyr Ser Asp Gly Ala Ser Ile
            425                 430                 435
```

```
Leu Pro Gln Leu Phe Asp Leu Ser Ser Asp Pro Asp Glu Leu Thr
            440                 445                 450
```

```
Asn Val Ala Val Lys Phe Pro Glu Ile Thr Tyr Ser Leu Asp Gln
            455                 460                 465
```

```
Lys Leu His Ser Ile Ile Asn Tyr Pro Lys Val Ser Ala Ser Val
            470                 475                 480
```

```
His Gln Tyr Asn Lys Glu Gln Phe Ile Lys Trp Lys Gln Ser Ile
            485                 490                 495
```

```
Gly Gln Asn Tyr Ser Asn Val Ile Ala Asn Leu Arg Trp His Gln
            500                 505                 510
```

```
Asp Trp Gln Lys Glu Pro Arg Lys Tyr Glu Asn Ala Ile Asp Gln
            515                 520                 525
```

```
Trp Leu Lys Thr His Met Asn Pro Arg Ala Val
            530                 535
```

```
<210> 133
<211> 1475
<212> DNA
<213> Homo sapiens

<400> 133
 gagagaagtc agcctggcag agagactctg aaatgaggga ttagaggtgt 50

 tcaaggagca agagcttcag cctgaagaca agggagcagt ccctgaagac 100

 gcttctactg agaggtctgc catggcctct cttggcctcc aacttgtggg 150

 ctacatccta ggccttctgg ggcttttggg cacactggtt gccatgctgc 200

 tccccagctg gaaaacaagt tcttatgtcg gtgccagcat tgtgacagca 250

 gttggcttct ccaagggcct ctggatggaa tgtgccacac acagcacagg 300

 catcacccag tgtgacatct atagcaccct tctgggcctg cccgctgaca 350

 tccaggctgc ccaggccatg atggtgacat ccagtgcaat ctcctccctg 400

 gcctgcatta tctctgtggt gggcatgaga tgcacagtct tctgccagga 450
```

142

```
atcccgagcc aaagacagag tggcggtagc aggtggagtc tttttcatcc 500

ttggaggcct cctgggattc attcctgttg cctggaatct tcatgggatc 550

ctacgggact tctactcacc actggtgcct gacagcatga aatttgagat 600

tggagaggct ctttacttgg gcattatttc ttccctgttc tccctgatag 650

ctggaatcat cctctgcttt tcctgctcat cccagagaaa tcgctccaac 700

tactacgatg cctaccaagc ccaacctctt gccacaagga gctctccaag 750

gcctggtcaa cctcccaaag tcaagagtga gttcaattcc tacagcctga 800

cagggtatgt gtgaagaacc aggggccaga gctggggggt ggctgggtct 850

gtgaaaaaca gtggacagca ccccgagggc cacaggtgag ggacactacc 900

actggatcgt gtcagaaggt gctgctgagg atagactgac tttggccatt 950

ggattgagca aaggcagaaa tgggggctag tgtaacagca tgcaggttga 1000

attgccaagg atgctcgcca tgccagcctt tctgttttcc tcaccttgct 1050

gctcccctgc cctaagtccc caaccctcaa cttgaaaccc cattccctta 1100

agccaggact cagaggatcc ctttgccctc tggtttacct gggactccat 1150

ccccaaaccc actaatcaca tcccactgac tgaccctctg tgatcaaaga 1200

ccctctctct ggctgaggtt ggctcttagc tcattgctgg ggatgggaag 1250

gagaagcagt ggcttttgtg ggcattgctc taacctactt ctcaagcttc 1300

cctccaaaga aactgattgg ccctggaacc tccatcccac tcttgttatg 1350

actccacagt gtccagacta atttgtgcat gaactgaaat aaaaccatcc 1400

tacggtatcc agggaacaga aagcaggatg caggatggga ggacaggaag 1450

gcagcctggg acatttaaaa aaata 1475
```

<210> 134
<211> 230
<212> PRT
<213> Homo sapiens

<400> 134

```
Met Ala Ser Leu Gly Leu Gln Leu Val Gly Tyr Ile Leu Gly Leu
 1               5                  10                      15

Leu Gly Leu Leu Gly Thr Leu Val Ala Met Leu Leu Pro Ser Trp
                20                  25                      30

Lys Thr Ser Ser Tyr Val Gly Ala Ser Ile Val Thr Ala Val Gly
                35                  40                      45

Phe Ser Lys Gly Leu Trp Met Glu Cys Ala Thr His Ser Thr Gly
```

143

Ile Thr Gln Cys Asp Ile Tyr Ser Thr Leu Leu Gly Leu Pro Ala
              65   70   75

Asp Ile Gln Ala Ala Gln Ala Met Met Val Thr Ser Ser Ala Ile
              80   85   90

Ser Ser Leu Ala Cys Ile Ile Ser Val Val Gly Met Arg Cys Thr
              95   100   105

Val Phe Cys Gln Glu Ser Arg Ala Lys Asp Arg Val Ala Val Ala
             110   115   120

Gly Gly Val Phe Phe Ile Leu Gly Gly Leu Leu Gly Phe Ile Pro
             125   130   135

Val Ala Trp Asn Leu His Gly Ile Leu Arg Asp Phe Tyr Ser Pro
             140   145   150

Leu Val Pro Asp Ser Met Lys Phe Glu Ile Gly Glu Ala Leu Tyr
             155   160   165

Leu Gly Ile Ile Ser Ser Leu Phe Ser Leu Ile Ala Gly Ile Ile
             170   175   180

Leu Cys Phe Ser Cys Ser Ser Gln Arg Asn Arg Ser Asn Tyr Tyr
             185   190   195

Asp Ala Tyr Gln Ala Gln Pro Leu Ala Thr Arg Ser Ser Pro Arg
             200   205   210

Pro Gly Gln Pro Pro Lys Val Lys Ser Glu Phe Asn Ser Tyr Ser
             215   220   225

Leu Thr Gly Tyr Val
             230

<210> 135
<211> 610
<212> DNA
<213> Homo sapiens

<400> 135
 gcactgctgc tgtcccatca gctgctctga agctccatgg tgcccagaat 50

 cttcgctcct gcttatgtgt cagtctgtct cctcctcttg tgtccaaggg 100

 aagtcatcgc tcccgctggc tcagaaccat ggctgtgcca gccggcaccc 150

 aggtgtggag acaagatcta caaccccttg gagcagtgct gttacaatga 200

 cgccatcgtg tccctgagcg agacccgcca atgtggtccc ccctgcacct 250

 tctggccctg ctttgagctc tgctgtcttg attcctttgg cctcacaaac 300

 gattttgttg tgaagctgaa ggttcagggt gtgaattccc agtgccactc 350

atctcccatc tccagtaaat gtgaaagcag aagacgtttt ccctgagaag 400

acatagaaag aaaatcaact ttcactaagg catctcagaa acataggcta 450

aggtaatatg tgtaccagta gagaagcctg aggaatttac aaaatgatgc 500

agctccaagc cattgtatgg cccatgtggg agactgatgg gacatggaga 550

atgacagtag attatcagga aataaataaa gtggttttc caatgtacac 600

acctgtaaaa 610

<210> 136
<211> 119
<212> PRT
<213> Homo sapiens

<400> 136
```
Met Val Pro Arg Ile Phe Ala Pro Ala Tyr Val Ser Val Cys Leu
 1               5                  10                  15

Leu Leu Leu Cys Pro Arg Glu Val Ile Ala Pro Ala Gly Ser Glu
                20                  25                  30

Pro Trp Leu Cys Gln Pro Ala Pro Arg Cys Gly Asp Lys Ile Tyr
                35                  40                  45

Asn Pro Leu Glu Gln Cys Cys Tyr Asn Asp Ala Ile Val Ser Leu
                50                  55                  60

Ser Glu Thr Arg Gln Cys Gly Pro Pro Cys Thr Phe Trp Pro Cys
                65                  70                  75

Phe Glu Leu Cys Cys Leu Asp Ser Phe Gly Leu Thr Asn Asp Phe
                80                  85                  90

Val Val Lys Leu Lys Val Gln Gly Val Asn Ser Gln Cys His Ser
                95                  100                 105

Ser Pro Ile Ser Ser Lys Cys Glu Ser Arg Arg Arg Phe Pro
                110                 115
```

<210> 137
<211> 771
<212> DNA
<213> Homo sapiens

<400> 137
ctccactgca accacccaga gccatggctc cccgaggctg catcgtagct 50

gtctttgcca ttttctgcat ctccaggctc ctctgctcac acggagcccc 100

agtggccccc atgactcctt acctgatgct gtgccagcca cacaagagat 150

gtggggacaa gttctacgac cccctgcagc actgttgcta tgatgatgcc 200

gtcgtgccct tggccaggac ccagacgtgt ggaaactgca ccttcagagt 250

145

```
ctgctttgag cagtgctgcc cctggacctt catggtgaag ctgataaacc 300

agaactgcga ctcagcccgg acctcggatg acaggctttg tcgcagtgtc 350

agctaatgga acatcagggg aacgatgact cctggattct ccttcctggg 400

tgggcctgga gaaagaggct ggtgttacct gagatctggg atgctgagtg 450

gctgtttggg ggccagagaa acacacactc aactgcccac ttcattctgt 500

gacctgtctg aggcccaccc tgcagctgcc ctgaggaggc ccacaggtcc 550

ccttctagaa ttctggacag catgagatgc gtgtgctgat gggggcccag 600

ggactctgaa ccctcctgat gaccccctatg gccaacatca acccggcacc 650

accccaaggc tggctgggga acccttcacc cttctgtgag attttccatc 700

atctcaagtt ctcttctatc caggagcaaa gcacaggatc ataataaatt 750

tatgtacttt ataaatgaaa a 771
```

<210> 138
<211> 110
<212> PRT
<213> Homo sapiens

<400> 138

```
Met Ala Pro Arg Gly Cys Ile Val Ala Val Phe Ala Ile Phe Cys
 1               5                  10                  15

Ile Ser Arg Leu Leu Cys Ser His Gly Ala Pro Val Ala Pro Met
                20                  25                  30

Thr Pro Tyr Leu Met Leu Cys Gln Pro His Lys Arg Cys Gly Asp
                35                  40                  45

Lys Phe Tyr Asp Pro Leu Gln His Cys Cys Tyr Asp Asp Ala Val
                50                  55                  60

Val Pro Leu Ala Arg Thr Gln Thr Cys Gly Asn Cys Thr Phe Arg
                65                  70                  75

Val Cys Phe Glu Gln Cys Cys Pro Trp Thr Phe Met Val Lys Leu
                ·80                 85                  90

Ile Asn Gln Asn Cys Asp Ser Ala Arg Thr Ser Asp Asp Arg Leu
                95                  100                 105

Cys Arg Ser Val Ser
                110
```

<210> 139
<211> 2044
<212> DNA
<213> Homo sapiens

<400> 139

146

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gggggcgggt gcctggagca cggcgctggg gccgcccgca gcgctcactc 50

gctcgcactc agtcgcggga ggcttccccg cgccggccgc gtcccgcccg 100

ctccccggca ccagaagttc ctctgcgcgt ccgacggcga catgggcgtc 150

cccacggccc tggaggccgg cagctggcgc tggggatccc tgctcttcgc 200

tctcttcctg gctgcgtccc taggtccggt ggcagccttc aaggtcgcca 250

cgccgtattc cctgtatgtc tgtcccgagg ggcagaacgt caccctcacc 300

tgcaggctct tgggccctgt ggacaaaggg cacgatgtga ccttctacaa 350

gacgtggtac cgcagctcga ggggcgaggt gcagacctgc tcagagcgcc 400

ggcccatccg caacctcacg ttccaggacc ttcacctgca ccatggaggc 450

caccaggctg ccaacaccag ccacgacctg gctcagcgcc acgggctgga 500

gtcggcctcc gaccaccatg gcaacttctc catcaccatg cgcaacctga 550

ccctgctgga tagcggcctc tactgctgcc tggtggtgga gatcaggcac 600

caccactcgg agcacagggt ccatggtgcc atggagctgc aggtgcagac 650

aggcaaagat gcaccatcca actgtgtggt gtacccatcc tcctcccagg 700

atagtgaaaa catcacggct gcagccctgg ctacgggtgc ctgcatcgta 750

ggaatcctct gcctccccct catcctgctc ctggtctaca agcaaaggca 800

ggcagcctcc aaccgccgtg cccaggagct ggtgcggatg gacagcaaca 850

ttcaagggat tgaaaacccc ggctttgaag cctcaccacc tgcccagggg 900

atacccgagg ccaaagtcag gcaccccctg tcctatgtgg cccagcggca 950

gccttctgag tctgggcggc atctgctttc ggagcccagc accccctgt 1000

ctcctccagg ccccggagac gtcttcttcc catccctgga ccctgtccct 1050

gactctccaa actttgaggt catctagccc agctggggga cagtgggctg 1100

ttgtggctgg gtctggggca ggtgcatttg agccagggct ggctctgtga 1150

gtggcctcct tggcctcggc cctggttccc tccctcctgc tctgggctca 1200

gatactgtga catcccagaa gcccagcccc tcaacccctc tggatgctac 1250

atggggatgc tggacggctc agcccctgtt ccaaggattt tggggtgctg 1300

agattctccc ctagagacct gaaattcacc agctacagat gccaaatgac 1350

ttacatctta agaagtctca gaacgtccag cccttcagca gctctcgttc 1400

tgagacatga gccttgggat gtggcagcat cagtgggaca agatggacac 1450
```

147

```
tgggccaccc tcccaggcac cagacacagg gcacggtgga gagacttctc 1500

ccccgtggcc gccttggctc ccccgttttg cccgaggctg ctcttctgtc 1550

agacttcctc tttgtaccac agtggctctg gggccaggcc tgcctgccca 1600

ctggccatcg ccaccttccc cagctgcctc ctaccagcag tttctctgaa 1650

gatctgtcaa caggttaagt caatctgggg cttccactgc ctgcattcca 1700

gtccccagag cttggtggtc ccgaaacggg aagtacatat tggggcatgg 1750

tggcctccgt gagcaaatgg tgtcttgggc aatctgaggc caggacagat 1800

gttgccccac ccactggaga tggtgctgag ggaggtgggt ggggccttct 1850

gggaaggtga gtggagaggg gcacctgccc cccgccctcc ccatccccta 1900

ctcccactgc tcagcgcggg ccattgcaag ggtgccacac aatgtcttgt 1950

ccaccctggg acacttctga gtatgaagcg ggatgctatt aaaaactaca 2000

tggggaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaga 2044
```

<210> 140
<211> 311
<212> PRT
<213> Homo sapiens

<400> 140

```
Met Gly Val Pro Thr Ala Leu Glu Ala Gly Ser Trp Arg Trp Gly
 1               5                  10                  15

Ser Leu Leu Phe Ala Leu Phe Leu Ala Ala Ser Leu Gly Pro Val
                20                  25                  30

Ala Ala Phe Lys Val Ala Thr Pro Tyr Ser Leu Tyr Val Cys Pro
                35                  40                  45

Glu Gly Gln Asn Val Thr Leu Thr Cys Arg Leu Leu Gly Pro Val
                50                  55                  60

Asp Lys Gly His Asp Val Thr Phe Tyr Lys Thr Trp Tyr Arg Ser
                65                  70                  75

Ser Arg Gly Glu Val Gln Thr Cys Ser Glu Arg Arg Pro Ile Arg
                80                  85                  90

Asn Leu Thr Phe Gln Asp Leu His Leu His His Gly Gly His Gln
                95                  100                 105

Ala Ala Asn Thr Ser His Asp Leu Ala Gln Arg His Gly Leu Glu
                110                 115                 120

Ser Ala Ser Asp His His Gly Asn Phe Ser Ile Thr Met Arg Asn
                125                 130                 135

Leu Thr Leu Leu Asp Ser Gly Leu Tyr Cys Cys Leu Val Val Glu
```

148

Ile Arg His His His Ser Glu His Arg Val His Gly Ala Met Glu
                    155   160   165

Leu Gln Val Gln Thr Gly Lys Asp Ala Pro Ser Asn Cys Val Val
                    170   175   180

Tyr Pro Ser Ser Ser Gln Asp Ser Glu Asn Ile Thr Ala Ala Ala
                    185   190   195

Leu Ala Thr Gly Ala Cys Ile Val Gly Ile Leu Cys Leu Pro Leu
                    200   205   210

Ile Leu Leu Leu Val Tyr Lys Gln Arg Gln Ala Ala Ser Asn Arg
                    215   220   225

Arg Ala Gln Glu Leu Val Arg Met Asp Ser Asn Ile Gln Gly Ile
                    230   235   240

Glu Asn Pro Gly Phe Glu Ala Ser Pro Pro Ala Gln Gly Ile Pro
                    245   250   255

Glu Ala Lys Val Arg His Pro Leu Ser Tyr Val Ala Gln Arg Gln
                    260   265   270

Pro Ser Glu Ser Gly Arg His Leu Leu Ser Glu Pro Ser Thr Pro
                    275   280   285

Leu Ser Pro Pro Gly Pro Gly Asp Val Phe Phe Pro Ser Leu Asp
                    290   295   300

Pro Val Pro Asp Ser Pro Asn Phe Glu Val Ile
                    305   310

<210> 141
<211> 1732
<212> DNA
<213> Homo sapiens

<400> 141
cccacgcgtc cgcgcctctc ccttctgctg gaccttcctt cgtctctcca 50

tctctccctc ctttccccgc gttctctttc caccttttctc ttcttcccac 100

cttagacctc ccttcctgcc ctcctttcct gcccaccgct gcttcctggc 150

ccttctccga ccccgctcta gcagcagacc tcctggggtc tgtgggttga 200

tctgtggccc ctgtgcctcc gtgtcctttt cgtctccctt cctcccgact 250

ccgctcccgg accagcggcc tgaccctggg gaaaggatgg ttcccgaggt 300

gagggtcctc tcctccttgc tgggactcgc gctgctctgg ttcccccctgg 350

actcccacgc tcgagcccgc ccagacatgt tctgcctttt ccatgggaag 400

agatactccc ccggcgagag ctggcacccc tacttggagc cacaaggcct 450

```
gatgtactgc ctgcgctgta cctgctcaga gggcgcccat gtgagttgtt 500

accgcctcca ctgtccgcct gtccactgcc cccagcctgt gacggagcca 550

cagcaatgct gtcccaagtg tgtggaacct cacactccct ctggactccg 600

ggccccacca aagtcctgcc agcacaacgg gaccatgtac caacacggag 650

agatcttcag tgcccatgag ctgttcccct cccgcctgcc caaccagtgt 700

gtcctctgca gctgcacaga gggccagatc tactgcggcc tcacaacctg 750

ccccgaacca ggctgcccag cacccctccc actgccagac tcctgctgcc 800

aagcctgcaa agatgaggca agtgagcaat cggatgaaga ggacagtgtg 850

cagtcgctcc atggggtgag acatcctcag gatccatgtt ccagtgatgc 900

tgggagaaag agaggcccgg gcaccccagc ccccactggc ctcagcgccc 950

ctctgagctt catccctcgc cacttcagac ccaagggagc aggcagcaca 1000

actgtcaaga tcgtcctgaa ggagaaacat aagaaagcct gtgtgcatgg 1050

cgggaagacg tactcccacg gggaggtgtg gcacccggcc ttccgtgcct 1100

tcggcccctt gccctgcatc ctatgcacct gtgaggatgg ccgccaggac 1150

tgccagcgtg tgacctgtcc caccgagtac ccctgccgtc accccgagaa 1200

agtggctggg aagtgctgca agatttgccc agaggacaaa gcagaccctg 1250

gccacagtga gatcagttct accaggtgtc ccaaggcacc gggccgggtc 1300

ctcgtccaca catcggtatc cccaagccca gacaacctgc gtcgctttgc 1350

cctggaacac gaggcctcgg acttggtgga gatctacctc tggaagctgg 1400

taaaagatga ggaaactgag gctcagagag gtgaagtacc tggcccaagg 1450

ccacacagcc agaatcttcc acttgactca gatcaagaaa gtcaggaagc 1500

aagacttcca gaaagaggca cagcacttcc gactgctcgc tggcccccac 1550

gaaggtcact ggaacgtctt cctagcccag accctggagc tgaaggtcac 1600

ggccagtcca gacaaagtga ccaagacata acaaagacct aacagttgca 1650

gatatgagct gtataattgt tgttattata tattaataaa taagaagttg 1700

cattaccctc aaaaaaaaaa aaaaaaaaaa aa 1732
```

<210> 142
<211> 451
<212> PRT
<213> Homo sapiens

<400> 142

150

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Met Val Pro Glu Val Arg Val Leu Ser Ser Leu Leu Gly Leu Ala
 1               5                   10                  15

Leu Leu Trp Phe Pro Leu Asp Ser His Ala Arg Ala Arg Pro Asp
                20                  25                  30

Met Phe Cys Leu Phe His Gly Lys Arg Tyr Ser Pro Gly Glu Ser
                35                  40                  45

Trp His Pro Tyr Leu Glu Pro Gln Gly Leu Met Tyr Cys Leu Arg
                50                  55                  60

Cys Thr Cys Ser Glu Gly Ala His Val Ser Cys Tyr Arg Leu His
                65                  70                  75

Cys Pro Pro Val His Cys Pro Gln Pro Val Thr Glu Pro Gln Gln
                80                  85                  90

Cys Cys Pro Lys Cys Val Glu Pro His Thr Pro Ser Gly Leu Arg
                95                  100                 105

Ala Pro Pro Lys Ser Cys Gln His Asn Gly Thr Met Tyr Gln His
                110                 115                 120

Gly Glu Ile Phe Ser Ala His Glu Leu Phe Pro Ser Arg Leu Pro
                125                 130                 135

Asn Gln Cys Val Leu Cys Ser Cys Thr Glu Gly Gln Ile Tyr Cys
                140                 145                 150

Gly Leu Thr Thr Cys Pro Glu Pro Gly Cys Pro Ala Pro Leu Pro
                155                 160                 165

Leu Pro Asp Ser Cys Cys Gln Ala Cys Lys Asp Glu Ala Ser Glu
                170                 175                 180

Gln Ser Asp Glu Glu Asp Ser Val Gln Ser Leu His Gly Val Arg
                185                 190                 195

His Pro Gln Asp Pro Cys Ser Ser Asp Ala Gly Arg Lys Arg Gly
                200                 205                 210

Pro Gly Thr Pro Ala Pro Thr Gly Leu Ser Ala Pro Leu Ser Phe
                215                 220                 225

Ile Pro Arg His Phe Arg Pro Lys Gly Ala Gly Ser Thr Thr Val
                230                 235                 240

Lys Ile Val Leu Lys Glu Lys His Lys Lys Ala Cys Val His Gly
                245                 250                 255

Gly Lys Thr Tyr Ser His Gly Glu Val Trp His Pro Ala Phe Arg
                260                 265                 270

Ala Phe Gly Pro Leu Pro Cys Ile Leu Cys Thr Cys Glu Asp Gly
                275                 280                 285

Arg Gln Asp Cys Gln Arg Val Thr Cys Pro Thr Glu Tyr Pro Cys
```

151

Arg His Pro Glu Lys Val Ala Gly Lys Cys Cys Lys Ile Cys Pro
              305   310   315

Glu Asp Lys Ala Asp Pro Gly His Ser Glu Ile Ser Ser Thr Arg
              320   325   330

Cys Pro Lys Ala Pro Gly Arg Val Leu Val His Thr Ser Val Ser
              335   340   345

Pro Ser Pro Asp Asn Leu Arg Arg Phe Ala Leu Glu His Glu Ala
              350   355   360

Ser Asp Leu Val Glu Ile Tyr Leu Trp Lys Leu Val Lys Asp Glu
              365   370   375

Glu Thr Glu Ala Gln Arg Gly Glu Val Pro Gly Pro Arg Pro His
              380   385   390

Ser Gln Asn Leu Pro Leu Asp Ser Asp Gln Glu Ser Gln Glu Ala
              395   400   405

Arg Leu Pro Glu Arg Gly Thr Ala Leu Pro Thr Ala Arg Trp Pro
              410   415   420

Pro Arg Arg Ser Leu Glu Arg Leu Pro Ser Pro Asp Pro Gly Ala
              425   430   435

Glu Gly His Gly Gln Ser Arg Gln Ser Asp Gln Asp Ile Thr Lys
              440   445   450

Thr

<210> 143
<211> 693
<212> DNA
<213> Homo sapiens

<400> 143
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  cggggagctc ccgtgggcgc tccgctggct gtgcaggcgg ccatggattc 100

  cttgcggaaa atgctgatct cagtcgcaat gctgggcgca ggggctggcg 150

  tgggctacgc gctcctcgtt atcgtgaccc cgggagagcg gcggaagcag 200

  gaaatgctaa aggagatgcc actgcaggac ccaaggagca gggaggaggc 250

  ggccaggacc cagcagctat tgctggccac tctgcaggag gcagcgacca 300

  cgcaggagaa cgtggcctgg aggaagaact ggatggttgg cggcgaaggc 350

  ggcgccagcg ggaggtcacc gtgagaccgg acttgcctcc gtgggcgccg 400

  gaccttggct tgggcgcagg aatccgaggc agcctttctc cttcgtgggc 450

ccagcggaga gtccggaccg agataccatg ccaggactct ccgggggtcct 500

gtgagctgcc gtcgggtgag cacgtttccc ccaaaccctg gactgactgc 550

tttaaggtcc gcaaggcggg ccagggccga gacgcgagtc ggatgtggtg 600

aactgaaaga accaataaaa tcatgttcct ccaaaaaaaa aaaaaaaaaa 650

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 693

<210> 144
<211> 93
<212> PRT
<213> Homo sapiens

<400> 144
Met Asp Ser Leu Arg Lys Met Leu Ile Ser Val Ala Met Leu Gly
1   5   10   15

Ala Gly Ala Gly Val Gly Tyr Ala Leu Leu Val Ile Val Thr Pro
            20   25   30

Gly Glu Arg Arg Lys Gln Glu Met Leu Lys Glu Met Pro Leu Gln
            35   40   45

Asp Pro Arg Ser Arg Glu Glu Ala Ala Arg Thr Gln Gln Leu Leu
            50   55   60

Leu Ala Thr Leu Gln Glu Ala Ala Thr Thr Gln Glu Asn Val Ala
            65   70   75

Trp Arg Lys Asn Trp Met Val Gly Gly Glu Gly Gly Ala Ser Gly
            80   85   90

Arg Ser Pro

<210> 145
<211> 1883
<212> DNA
<213> Homo sapiens

<400> 145
caggagagaa ggcaccgccc ccacccccgcc tccaaagcta accctcgggc 50

ttgagggggaa gaggctgact gtacgttcct tctactctgg caccactctc 100

caggctgcca tggggcccag caccccctctc ctcatcttgt tccttttgtc 150

atggtcggga cccctccaag gacagcagca ccaccttgtg gagtacatgg 200

aacgccgact agctgcttta gaggaacggc tggcccagtg ccaggaccag 250

agtagtcggc atgctgctga gctgcgggac ttcaagaaca gatgctgcc 300

actgctggag gtggcagaga aggagcggga ggcactcaga actgaggccg 350

acaccatctc cgggagagtg gatcgtctgg agcgggaggt agactatctg 400

```
gagacccaga acccagctct gccctgtgta gagtttgatg agaaggtgac 450

tggaggccct gggaccaaag gcaagggaag aaggaatgag aagtacgata 500

tggtgacaga ctgtggctac acaatctctc aagtgagatc aatgaagatt 550

ctgaagcgat ttggtggccc agctggtcta tggaccaagg atccactggg 600

gcaaacagag aagatctacg tgttagatgg gacacagaat gacacagcct 650

ttgtcttccc aaggctgcgt gacttcaccc ttgccatggc tgcccggaaa 700

gcttcccgag tccgggtgcc cttcccctgg gtaggcacag ggcagctggt 750

atatggtggc tttctttatt ttgctcggag gcctcctgga agacctggtg 800

gaggtggtga gatggagaac actttgcagc taatcaaatt ccacctggca 850

aaccgaacag tggtggacag ctcagtattc ccagcagagg ggctgatccc 900

cccctacggc ttgacagcag acacctacat cgacctggta gctgatgagg 950

aaggtctttg ggctgtctat gccacccggg aggatgacag gcacttgtgt 1000

ctggccaagt tagatccaca gacactggac acagagcagc agtgggacac 1050

accatgtccc agagagaatg ctgaggctgc ctttgtcatc tgtgggaccc 1100

tctatgtcgt ctataacacc cgtcctgcca gtcgggcccg catccagtgc 1150

tcctttgatg ccagcggcac cctgacccct gaacgggcag cactccctta 1200

ttttccccgc agatatggtg cccatgccag cctccgctat aacccccgag 1250

aacgccagct ctatgcctgg gatgatggct accagattgt ctataagctg 1300

gagatgagga agaaagagga ggaggtttga ggagctagcc ttgttttttg 1350

catctttctc actcccatac atttatatta tatccccact aaatttcttg 1400

ttcctcattc ttcaaatgtg ggccagttgt ggctcaaatc ctctatattt 1450

ttagccaatg gcaatcaaat tctttcagct cctttgtttc atacggaact 1500

ccagatcctg agtaatcctt ttagagcccg aagagtcaaa accctcaatg 1550

ttccctcctg ctctcctgcc ccatgtcaac aaatttcagg ctaaggatgc 1600

cccagaccca gggctctaac cttgtatgcg ggcaggccca gggagcaggc 1650

agcagtgttc ttcccctcag agtgacttgg ggagggagaa ataggaggag 1700

acgtccagct ctgtcctctc ttcctcactc ctcccttcag tgtcctgagg 1750

aacaggactt tctccacatt gttttgtatt gcaacatttt gcattaaaag 1800

gaaaatccac aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1850
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154

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 1883

<210> 146
<211> 406
<212> PRT
<213> Homo sapiens

<400> 146
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Met Gly Pro Ser Thr Pro Leu Leu Ile Leu Phe Leu Leu Ser Trp
 1               5                  10                  15

Ser Gly Pro Leu Gln Gly Gln Gln His His Leu Val Glu Tyr Met
               20                  25                  30

Glu Arg Arg Leu Ala Ala Leu Glu Glu Arg Leu Ala Gln Cys Gln
               35                  40                  45

Asp Gln Ser Ser Arg His Ala Ala Glu Leu Arg Asp Phe Lys Asn
               50                  55                  60

Lys Met Leu Pro Leu Leu Glu Val Ala Glu Lys Glu Arg Glu Ala
               65                  70                  75

Leu Arg Thr Glu Ala Asp Thr Ile Ser Gly Arg Val Asp Arg Leu
               80                  85                  90

Glu Arg Glu Val Asp Tyr Leu Glu Thr Gln Asn Pro Ala Leu Pro
               95                 100                 105

Cys Val Glu Phe Asp Glu Lys Val Thr Gly Gly Pro Gly Thr Lys
              110                 115                 120

Gly Lys Gly Arg Arg Asn Glu Lys Tyr Asp Met Val Thr Asp Cys
              125                 130                 135

Gly Tyr Thr Ile Ser Gln Val Arg Ser Met Lys Ile Leu Lys Arg
              140                 145                 150

Phe Gly Gly Pro Ala Gly Leu Trp Thr Lys Asp Pro Leu Gly Gln
              155                 160                 165

Thr Glu Lys Ile Tyr Val Leu Asp Gly Thr Gln Asn Asp Thr Ala
              170                 175                 180

Phe Val Phe Pro Arg Leu Arg Asp Phe Thr Leu Ala Met Ala Ala
              185                 190                 195

Arg Lys Ala Ser Arg Val Arg Val Pro Phe Pro Trp Val Gly Thr
              200                 205                 210

Gly Gln Leu Val Tyr Gly Gly Phe Leu Tyr Phe Ala Arg Arg Pro
              215                 220                 225

Pro Gly Arg Pro Gly Gly Gly Gly Glu Met Glu Asn Thr Leu Gln
              230                 235                 240

Leu Ile Lys Phe His Leu Ala Asn Arg Thr Val Val Asp Ser Ser
              245                 250                 255
```

155

```
Val Phe Pro Ala Glu Gly Leu Ile Pro Pro Tyr Gly Leu Thr Ala
            260                 265                 270

Asp Thr Tyr Ile Asp Leu Val Ala Asp Glu Glu Gly Leu Trp Ala
            275                 280                 285

Val Tyr Ala Thr Arg Glu Asp Asp Arg His Leu Cys Leu Ala Lys
            290                 295                 300

Leu Asp Pro Gln Thr Leu Asp Thr Glu Gln Gln Trp Asp Thr Pro
            305                 310                 315

Cys Pro Arg Glu Asn Ala Glu Ala Ala Phe Val Ile Cys Gly Thr
            320                 325                 330

Leu Tyr Val Val Tyr Asn Thr Arg Pro Ala Ser Arg Ala Arg Ile
            335                 340                 345

Gln Cys Ser Phe Asp Ala Ser Gly Thr Leu Thr Pro Glu Arg Ala
            350                 355                 360

Ala Leu Pro Tyr Phe Pro Arg Arg Tyr Gly Ala His Ala Ser Leu
            365                 370                 375

Arg Tyr Asn Pro Arg Glu Arg Gln Leu Tyr Ala Trp Asp Asp Gly
            380                 385                 390

Tyr Gln Ile Val Tyr Lys Leu Glu Met Arg Lys Lys Glu Glu Glu
            395                 400                 405

Val
```

<210> 147
<211> 2052
<212> DNA
<213> Homo sapiens

<400> 147
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ccgctcacgc agagcctctc cgtggcttcc gcaccttgag cattaggcca  100

gttctcctct tctctctaat ccatccgtca cctctcctgt catccgtttc  150

catgccgtga ggtccattca cagaacacat ccatggctct catgctcagt  200

ttggttctga gtctcctcaa gctgggatca gggcagtggc aggtgtttgg  250

gccagacaag cctgtccagg ccttggtggg ggaggacgca gcattctcct  300

gtttcctgtc tcctaagacc aatgcagagg ccatggaagt gcggttcttc  350

aggggccagt tctctagcgt ggtccacctc tacagggacg ggaaggacca  400

gccatttatg cagatgccac agtatcaagg caggacaaaa ctggtgaagg  450

attctattgc ggaggggcgc atctctctga ggctggaaaa cattactgtg  500
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ttggatgctg gcctctatgg gtgcaggatt agttcccagt cttactacca 550

gaaggccatc tgggagctac aggtgtcagc actgggctca gttcctctca 600

tttccatcac gggatatgtt gatagagaca tccagctact ctgtcagtcc 650

tcgggctggt tcccccggcc cacagcgaag tggaaaggtc cacaaggaca 700

ggatttgtcc acagactcca ggacaaacag agacatgcat ggcctgtttg 750

atgtggagat ctctctgacc gtccaagaga acgccgggag catatcctgt 800

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aggagatacc tttttcgagc ctatatcgtg gcacctggct accaaagtac 900

tgggaatact ctgctgtggc ctattttttg gcattgttgg actgaagatt 950

ttcttctcca aattccagtg gaaaatccag gcggaactgg actggagaag 1000

aaagcacgga caggcagaat tgagagacgc ccggaaacac gcagtggagg 1050

tgactctgga tccagagacg gctcacccga agctctgcgt ttctgatctg 1100

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atgggagtca ggtgtcatgg ctgccctgag ctgggaggga agaaggctga 1850

cattacattt agtttgctct cactccatct ggctaagtga tcttgaaata 1900

ccacctctca ggtgaagaac cgtcaggaat tcccatctca caggctgtgg 1950
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157

tgtagattaa gtagacaagg aatgtgaata atgcttagat cttattgatg 2000

acagagtgta tcctaatggt ttgttcatta tattacactt tcagtaaaaa 2050

aa 2052

<210> 148
<211> 500
<212> PRT
<213> Homo sapiens

<400> 148

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Met Ala Leu Met Leu Ser Leu Val Leu Ser Leu Leu Lys Leu Gly
 1               5                  10                  15

Ser Gly Gln Trp Gln Val Phe Gly Pro Asp Lys Pro Val Gln Ala
                20                  25                  30

Leu Val Gly Glu Asp Ala Ala Phe Ser Cys Phe Leu Ser Pro Lys
                35                  40                  45

Thr Asn Ala Glu Ala Met Glu Val Arg Phe Phe Arg Gly Gln Phe
                50                  55                  60

Ser Ser Val Val His Leu Tyr Arg Asp Gly Lys Asp Gln Pro Phe
                65                  70                  75

Met Gln Met Pro Gln Tyr Gln Gly Arg Thr Lys Leu Val Lys Asp
                80                  85                  90

Ser Ile Ala Glu Gly Arg Ile Ser Leu Arg Leu Glu Asn Ile Thr
                95                 100                 105

Val Leu Asp Ala Gly Leu Tyr Gly Cys Arg Ile Ser Ser Gln Ser
               110                 115                 120

Tyr Tyr Gln Lys Ala Ile Trp Glu Leu Gln Val Ser Ala Leu Gly
               125                 130                 135

Ser Val Pro Leu Ile Ser Ile Thr Gly Tyr Val Asp Arg Asp Ile
               140                 145                 150

Gln Leu Leu Cys Gln Ser Ser Gly Trp Phe Pro Arg Pro Thr Ala
               155                 160                 165

Lys Trp Lys Gly Pro Gln Gly Gln Asp Leu Ser Thr Asp Ser Arg
               170                 175                 180

Thr Asn Arg Asp Met His Gly Leu Phe Asp Val Glu Ile Ser Leu
               185                 190                 195

Thr Val Gln Glu Asn Ala Gly Ser Ile Ser Cys Ser Met Arg His
               200                 205                 210

Ala His Leu Ser Arg Glu Val Glu Ser Arg Val Gln Ile Gly Asp
               215                 220                 225

Thr Phe Phe Glu Pro Ile Ser Trp His Leu Ala Thr Lys Val Leu
```

158

			230				235				240

Gly Ile Leu Cys Cys Gly Leu Phe Phe Gly Ile Val Gly Leu Lys
                245   250   255

Ile Phe Phe Ser Lys Phe Gln Trp Lys Ile Gln Ala Glu Leu Asp
                260   265   270

Trp Arg Arg Lys His Gly Gln Ala Glu Leu Arg Asp Ala Arg Lys
                275   280   285

His Ala Val Glu Val Thr Leu Asp Pro Glu Thr Ala His Pro Lys
                290   295   300

Leu Cys Val Ser Asp Leu Lys Thr Val Thr His Arg Lys Ala Pro
                305   310   315

Gln Glu Val Pro His Ser Glu Lys Arg Phe Thr Arg Lys Ser Val
                320   325   330

Val Ala Ser Gln Ser Phe Gln Ala Gly Lys His Tyr Trp Glu Val
                335   340   345

Asp Gly Gly His Asn Lys Arg Trp Arg Val Gly Val Cys Arg Asp
                350   355   360

Asp Val Asp Arg Arg Lys Glu Tyr Val Thr Leu Ser Pro Asp His
                365   370   375

Gly Tyr Trp Val Leu Arg Leu Asn Gly Glu His Leu Tyr Phe Thr
                380   385   390

Leu Asn Pro Arg Phe Ile Ser Val Phe Pro Arg Thr Pro Pro Thr
                395   400   405

Lys Ile Gly Val Phe Leu Asp Tyr Glu Cys Gly Thr Ile Ser Phe
                410   415   420

Phe Asn Ile Asn Asp Gln Ser Leu Ile Tyr Thr Leu Thr Cys Arg
                425   430   435

Phe Glu Gly Leu Leu Arg Pro Tyr Ile Glu Tyr Pro Ser Tyr Asn
                440   445   450

Glu Gln Asn Gly Thr Pro Ile Val Ile Cys Pro Val Thr Gln Glu
                455   460   465

Ser Glu Lys Glu Ala Ser Trp Gln Arg Ala Ser Ala Ile Pro Glu
                470   475   480

Thr Ser Asn Ser Glu Ser Ser Ser Gln Ala Thr Thr Pro Phe Leu
                485   490   495

Pro Arg Gly Glu Met
                500

<210> 149
<211> 24

159

<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 149
 gcgtggtcca cctctacagg gacg 24

<210> 150
<211> 23
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-23
<223> Synthetic construct.

<400> 150
 ggaactgacc cagtgctgac acc 23

<210> 151
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 151
 gcagatgcca cagtatcaag gcaggacaaa actggtgaag gattc 45

<210> 152
<211> 2294
<212> DNA
<213> Homo sapiens

<400> 152
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 aatgaatggc ggagccgagc gcgccatgag gagcctgccg agcctgggcg 150

 gcctcgccct gttgtgctgc gccgccgccg ccgccgccgt cgcctcagcc 200

 gcctcggcgg ggaatgtcac cggtggcggc ggggccgcgg ggcaggtgga 250

 cgcgtcgccg ggccccgggt tgcggggcga gcccagccac cccttcccta 300

 gggcgacggc tcccacggcc caggccccga ggaccgggcc cccgcgcgcc 350

 accgtccacc gacccctggc tgcgacttct ccagcccagt ccccggagac 400

160

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caccccctctt tgggcgactg ctggaccctc ttccaccacc tttcaggcgc 450

cgctcggccc ctcgccgacc accctccgg cggcggaacg cacttcgacc 500

acctctcagg cgccgaccag acccgcgccg accacccttt cgacgaccac 550

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ctccccggac cccgaccccc gatctcccca gcagcagcaa cagcagcgtc 650

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tgtatgtaac tgctctgtgg ttggaagcct gaatgtgaat cgctgcaacc 750

agaccacagg gcagtgtgag tgtcggccag gttatcaggg cttcactgt 800

gaaacctgca aagagggctt ttacctaaat tacacttctg ggctctgtca 850

gccatgtgac tgtagtccac atggagctct cagcataccg tgcaacaggt 900

aagcaacaga gggtggaact gaagtttatt ttattttagc aagggaaaaa 950

aaaaggctgc tactctcaag gaccatactg gtttaaacaa aggaggatga 1000

gggtcataga tttacaaaat attttatata cttttattct cttactttat 1050

atgttatatt taatgtcagg atttaaaaac atctaattta ctgatttagt 1100

tcttcaaaag cactagagtc gccaattttt ctctgggata atttctgtaa 1150

atttcatggg aaaaaattat tgaagaataa atctgctttc tggaagggct 1200

ttcaggcatg aaacctgcta ggaggtttag aaatgttctt atgtttatta 1250

atataccatt ggagtttgag gaaatttgtt gtttggttta tttttctctc 1300

taatcaaaat tctacatttg tttctttgga catctaaagc ttaacctggg 1350

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taccagtaca tttttgagac caaaagtaga ttaagcagga attatcttta 1450

aactattatg ttatttggag gtaatttaat ctagtggaat aatgtactgt 1500

tatctaagca tttgccttgt actgcactga aagtaattat tctttgacct 1550

tatgtgaggc acttggcttt ttgtggaccc caagtcaaaa aactgaagag 1600

acagtattaa ataatgaaaa aaataatgac aggttatact cagtgtaacc 1650

tgggtataac ccaagatctg ctgccactta cgagctgtgt ccttgggca 1700

agtaatttcc tttcactgag cttgtttctt ctcaaggttg ttgtgaagat 1750

taaatgagtt gatatatata aaatgcctag cacatgtcac tcaataaatt 1800

ctggtttgtt ttaatttcaa aggaatatta tggactgaaa tgagagaaca 1850
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161

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tgttttaaga acttttagct ccttgacaaa gaagtgcttt atactttagc 1900

actaaatatt ttaaatgctt tataaatgat attatactgt tatggaatat 1950

tgtatcatat tgtagtttat taaaaatgta gaagaggctg ggcgcggtgg 2000

ctcacgcctg taatcctagc actttgggag gccaaggcgg gtggatcact 2050

tgaggccagg agttctagat gagcctggcc agcacagtga aaccccgtct 2100

ctactaaaaa tacaaacaaa ttagctgggc gtggtggcac acacctgtag 2150

tcccagctac tcgggaggct gaggcaggag aatcggttga acccgggagg 2200

tggaggttgc agtgagctga gatcgcgcca ctgcactcca gcctggtgag 2250

agagggagac tctgtcttaa aaaaaaaaa aaaaaaaaa aaaa 2294
```

<210> 153
<211> 258
<212> PRT
<213> Homo sapiens

<400> 153
```
Met Arg Ser Leu Pro Ser Leu Gly Gly Leu Ala Leu Leu Cys Cys
  1               5                  10                  15

Ala Ala Ala Ala Ala Ala Val Ala Ser Ala Ala Ser Ala Gly Asn
                 20                  25                  30

Val Thr Gly Gly Gly Gly Ala Ala Gly Gln Val Asp Ala Ser Pro
                 35                  40                  45

Gly Pro Gly Leu Arg Gly Glu Pro Ser His Pro Phe Pro Arg Ala
                 50                  55                  60

Thr Ala Pro Thr Ala Gln Ala Pro Arg Thr Gly Pro Pro Arg Ala
                 65                  70                  75

Thr Val His Arg Pro Leu Ala Ala Thr Ser Pro Ala Gln Ser Pro
                 80                  85                  90

Glu Thr Thr Pro Leu Trp Ala Thr Ala Gly Pro Ser Ser Thr Thr
                 95                 100                 105

Phe Gln Ala Pro Leu Gly Pro Ser Pro Thr Thr Pro Pro Ala Ala
                110                 115                 120

Glu Arg Thr Ser Thr Thr Ser Gln Ala Pro Thr Arg Pro Ala Pro
                125                 130                 135

Thr Thr Leu Ser Thr Thr Thr Gly Pro Ala Pro Thr Thr Pro Val
                140                 145                 150

Ala Thr Thr Val Pro Ala Pro Thr Thr Pro Arg Thr Pro Thr Pro
                155                 160                 165

Asp Leu Pro Ser Ser Ser Asn Ser Ser Val Leu Pro Thr Pro Pro
```

162

```
                   170                     175                      180
  Ala Thr Glu Ala Pro Ser Ser Pro Pro Pro Glu Tyr Val Cys Asn
                   185                     190                      195
  Cys Ser Val Val Gly Ser Leu Asn Val Asn Arg Cys Asn Gln Thr
                   200                     205                      210
  Thr Gly Gln Cys Glu Cys Arg Pro Gly Tyr Gln Gly Leu His Cys
                   215                     220                      225
  Glu Thr Cys Lys Glu Gly Phe Tyr Leu Asn Tyr Thr Ser Gly Leu
                   230                     235                      240
  Cys Gln Pro Cys Asp Cys Ser Pro His Gly Ala Leu Ser Ile Pro
                   245                     250                      255
  Cys Asn Arg
```

<210> 154
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 154
 aactgctctg tggttggaag cctg 24

<210> 155
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 155
 cagtcacatg gctgacagac ccac 24

<210> 156
<211> 38
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-38
<223> Synthetic construct.

<400> 156
 aggttatcag gggcttcact gtgaaacctg caaagagg 38

<210> 157
<211> 689
<212> DNA
<213> Homo sapiens

<400> 157
tgcggcgcag tgtagacctg ggaggatggg cggcctgctg ctggctgctt 50

ttctggcttt ggtctcggtg cccagggccc aggccgtgtg gttgggaaga 100

ctggaccctg agcagcttct tgggccctgg tacgtgcttg cggtggcctc 150

ccgggaaaag ggctttgcca tggagaagga catgaagaac gtcgtggggg 200

tggtggtgac cctcactcca gaaaacaacc tgcggacgct gtcctctcag 250

cacgggctgg gagggtgtga ccagagtgtc atggacctga taaagcgaaa 300

ctccggatgg gtgtttgaga tccctcaat aggcgtgctg gagctctggg 350

tgctggccac caacttcaga gactatgcca tcatcttcac tcagctggag 400

ttcggggacg agcccttcaa caccgtggag ctgtacagtc tgacggagac 450

agccagccag gaggccatgg ggctcttcac caagtggagc aggagcctgg 500

gcttcctgtc acagtagcag gcccagctgc agaaggacct cacctgtgct 550

cacaagatcc ttctgtgagt gctgcgtccc cagtagggat ggcgcccaca 600

gggtcctgtg acctcggcca gtgtccaccc acctcgctca gcggctcccg 650

gggcccagca ccagctcaga ataaagcgat tccacagca 689

<210> 158
<211> 163
<212> PRT
<213> Homo sapiens

<400> 158
Met Gly Gly Leu Leu Leu Ala Ala Phe Leu Ala Leu Val Ser Val
1   5   10   15

Pro Arg Ala Gln Ala Val Trp Leu Gly Arg Leu Asp Pro Glu Gln
                20   25   30

Leu Leu Gly Pro Trp Tyr Val Leu Ala Val Ala Ser Arg Glu Lys
                35   40   45

Gly Phe Ala Met Glu Lys Asp Met Lys Asn Val Val Gly Val Val
                50   55   60

Val Thr Leu Thr Pro Glu Asn Asn Leu Arg Thr Leu Ser Ser Gln
                65   70   75

His Gly Leu Gly Gly Cys Asp Gln Ser Val Met Asp Leu Ile Lys
                80   85   90

164

```
Arg Asn Ser Gly Trp Val Phe Glu Asn Pro Ser Ile Gly Val Leu
            95                  100                 105

Glu Leu Trp Val Leu Ala Thr Asn Phe Arg Asp Tyr Ala Ile Ile
            110                 115                 120

Phe Thr Gln Leu Glu Phe Gly Asp Glu Pro Phe Asn Thr Val Glu
            125                 130                 135

Leu Tyr Ser Leu Thr Glu Thr Ala Ser Gln Glu Ala Met Gly Leu
            140                 145                 150

Phe Thr Lys Trp Ser Arg Ser Leu Gly Phe Leu Ser Gln
            155                 160
```

<210> 159
<211> 1665
<212> DNA
<213> Homo sapiens

<400> 159
```
aacagacgtt ccctcgcggc cctggcacct ctaaccccag acatgctgct 50

gctgctgctg cccctgctct gggggaggga gagggcggaa ggacagacaa 100

gtaaactgct gacgatgcag agttccgtga cggtgcagga aggcctgtgt 150

gtccatgtgc cctgctcctt ctcctacccc tcgcatggct ggatttaccc 200

tggcccagta gttcatggct actggttccg ggaaggggcc aatacagacc 250

aggatgctcc agtggccaca aacaacccag ctcgggcagt gtgggaggag 300

actcgggacc gattccacct ccttggggac ccacatacca agaattgcac 350

cctgagcatc agagatgcca gaagaagtga tgcgggggaga tacttctttc 400

gtatggagaa aggaagtata aaatggaatt ataaacatca ccggctctct 450

gtgaatgtga cagccttgac ccacaggccc aacatcctca tcccaggcac 500

cctggagtcc ggctgccccc agaatctgac ctgctctgtg ccctgggcct 550

gtgagcaggg dacacccccct atgatctcct ggatagggac ctccgtgtcc 600

cccctggacc cctccaccac ccgctcctcg gtgctcaccc tcatcccaca 650

gccccaggac catggcacca gcctcacctg tcaggtgacc ttccctgggg 700

ccagcgtgac cacgaacaag accgtccatc tcaacgtgtc ctacccgcct 750

cagaacttga ccatgactgt cttccaagga dacggcacag tatccacagt 800

cttgggaaat ggctcatctc tgtcactccc agagggccag tctctgcgcc 850

tggtctgtgc agttgatgca gttgacagca atccccctgc caggctgagc 900

ctgagctgga gaggcctgac cctgtgcccc tcacagccct caaacccggg 950
```

165
```

```
ggtgctggag ctgccttggg tgcacctgag ggatgcagct gaattcacct 1000

gcagagctca gaaccctctc ggctctcagc aggtctacct gaacgtctcc 1050

ctgcagagca aagccacatc aggagtgact caggggtgg tcggggagc 1100

tggagccaca gccctggtct tcctgtcctt ctgcgtcatc ttcgttgtag 1150

tgaggtcctg caggaagaaa tcggcaaggc cagcagcggg cgtgggagat 1200

acgggcatag aggatgcaaa cgctgtcagg ggttcagcct ctcaggggcc 1250

cctgactgaa ccttgggcag aagacagtcc cccagaccag cctcccccag 1300

cttctgcccg ctcctcagtg ggggaaggag agctccagta tgcatccctc 1350

agcttccaga tggtgaagcc ttgggactcg cggggacagg aggccactga 1400

caccgagtac tcggagatca agatccacag atgagaaact gcagagactc 1450

accctgattg agggatcaca gcccctccag gcaagggaga agtcagaggc 1500

tgattcttgt agaattaaca gccctcaacg tgatgagcta tgataacact 1550

atgaattatg tgcagagtga aaagcacaca ggctttagag tcaaagtatc 1600

tcaaacctga atccacactg tgccctccct tttattttt taactaaaag 1650

acagacaaat tccta 1665
```

<210> 160
<211> 463
<212> PRT
<213> Homo sapiens

<400> 160

```
Met Leu Leu Leu Leu Pro Leu Leu Trp Gly Arg Glu Arg Ala
 1               5                  10                  15

Glu Gly Gln Thr Ser Lys Leu Leu Thr Met Gln Ser Ser Val Thr
                 20                  25                  30

Val Gln Glu Gly Leu Cys Val His Val Pro Cys Ser Phe Ser Tyr
                 35                  40                  45

Pro Ser His Gly Trp Ile Tyr Pro Gly Pro Val Val His Gly Tyr
                 50                  55                  60

Trp Phe Arg Glu Gly Ala Asn Thr Asp Gln Asp Ala Pro Val Ala
                 65                  70                  75

Thr Asn Asn Pro Ala Arg Ala Val Trp Glu Glu Thr Arg Asp Arg
                 80                  85                  90

Phe His Leu Leu Gly Asp Pro His Thr Lys Asn Cys Thr Leu Ser
                 95                  100                 105

Ile Arg Asp Ala Arg Arg Ser Asp Ala Gly Arg Tyr Phe Phe Arg
```

166

```
                  110                    115                    120
Met Glu Lys Gly Ser Ile Lys Trp Asn Tyr Lys His His Arg Leu
                125                    130                    135

Ser Val Asn Val Thr Ala Leu Thr His Arg Pro Asn Ile Leu Ile
                140                    145                    150

Pro Gly Thr Leu Glu Ser Gly Cys Pro Gln Asn Leu Thr Cys Ser
                155                    160                    165

Val Pro Trp Ala Cys Glu Gln Gly Thr Pro Pro Met Ile Ser Trp
                170                    175                    180

Ile Gly Thr Ser Val Ser Pro Leu Asp Pro Ser Thr Thr Arg Ser
                185                    190                    195

Ser Val Leu Thr Leu Ile Pro Gln Pro Gln Asp His Gly Thr Ser
                200                    205                    210

Leu Thr Cys Gln Val Thr Phe Pro Gly Ala Ser Val Thr Thr Asn
                215                    220                    225

Lys Thr Val His Leu Asn Val Ser Tyr Pro Pro Gln Asn Leu Thr
                230                    235                    240

Met Thr Val Phe Gln Gly Asp Gly Thr Val Ser Thr Val Leu Gly
                245                    250                    255

Asn Gly Ser Ser Leu Ser Leu Pro Glu Gly Gln Ser Leu Arg Leu
                260                    265                    270

Val Cys Ala Val Asp Ala Val Asp Ser Asn Pro Pro Ala Arg Leu
                275                    280                    285

Ser Leu Ser Trp Arg Gly Leu Thr Leu Cys Pro Ser Gln Pro Ser
                290                    295                    300

Asn Pro Gly Val Leu Glu Leu Pro Trp Val His Leu Arg Asp Ala
                305                    310                    315

Ala Glu Phe Thr Cys Arg Ala Gln Asn Pro Leu Gly Ser Gln Gln
                320                    325                    330

Val Tyr Leu Asn Val Ser Leu Gln Ser Lys Ala Thr Ser Gly Val
                335                    340                    345

Thr Gln Gly Val Val Gly Gly Ala Gly Ala Thr Ala Leu Val Phe
                350                    355                    360

Leu Ser Phe Cys Val Ile Phe Val Val Val Arg Ser Cys Arg Lys
                365                    370                    375

Lys Ser Ala Arg Pro Ala Ala Gly Val Gly Asp Thr Gly Ile Glu
                380                    385                    390

Asp Ala Asn Ala Val Arg Gly Ser Ala Ser Gln Gly Pro Leu Thr
                395                    400                    405
```

167

```
Glu Pro Trp Ala Glu Asp Ser Pro Pro Asp Gln Pro Pro Pro Ala
            410             415             420

Ser Ala Arg Ser Ser Val Gly Glu Gly Glu Leu Gln Tyr Ala Ser
            425             430             435

Leu Ser Phe Gln Met Val Lys Pro Trp Asp Ser Arg Gly Gln Glu
            440             445             450

Ala Thr Asp Thr Glu Tyr Ser Glu Ile Lys Ile His Arg
            455             460
```

<210> 161
<211> 739
<212> DNA
<213> Homo sapiens

<400> 161

```
gacgcccagt gacctgccga ggtcggcagc acagagctct ggagatgaag 50

accctgttcc tgggtgtcac gctcggcctg gccgctgccc tgtccttcac 100

cctggaggag gaggatatca cagggacctg gtacgtgaag gccatggtgg 150

tcgataagga ctttccggag gacaggaggc ccaggaaggt gtccccagtg 200

aaggtgacag ccctgggcgg tgggaagttg gaagccacgt tcaccttcat 250

gagggaggat cggtgcatcc agaagaaaat cctgatgcgg aagacggagg 300

agcctggcaa atacagcgcc tatggggca ggaagctcat gtacctgcag 350

gagctgccca ggagggacca ctacatcttt tactgcaaag accagcacca 400

tggggggctg ctccacatgg gaaagcttgt gggtaggaat tctgatacca 450

accgggaggc cctggaagaa tttaagaaat tggtgcagcg caagggactc 500

tcggaggagg acattttcac gccccctgcag acgggaagct gcgttcccga 550

acactaggca gccccgggt ctgcacctcc agagcccacc ctaccaccag 600

acacagagcc cggaccacct ggacctaccc tccagccatg acccttccct 650

gctcccaccc acctgactcc aaataaagtc cttttccccc aaaaaaaaaa 700

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaa 739
```

<210> 162
<211> 170
<212> PRT
<213> Homo sapiens

<400> 162

```
Met Lys Thr Leu Phe Leu Gly Val Thr Leu Gly Leu Ala Ala Ala
  1               5               10              15

Leu Ser Phe Thr Leu Glu Glu Glu Asp Ile Thr Gly Thr Trp Tyr
```

168

```
                    20                    25                    30
    Val Lys Ala Met Val Val Asp Lys Asp Phe Pro Glu Asp Arg Arg
                    35                    40                    45

    Pro Arg Lys Val Ser Pro Val Lys Val Thr Ala Leu Gly Gly Gly
                    50                    55                    60

    Lys Leu Glu Ala Thr Phe Thr Phe Met Arg Glu Asp Arg Cys Ile
                    65                    70                    75

    Gln Lys Lys Ile Leu Met Arg Lys Thr Glu Glu Pro Gly Lys Tyr
                    80                    85                    90

    Ser Ala Tyr Gly Gly Arg Lys Leu Met Tyr Leu Gln Glu Leu Pro
                    95                    100                   105

    Arg Arg Asp His Tyr Ile Phe Tyr Cys Lys Asp Gln His His Gly
                    110                   115                   120

    Gly Leu Leu His Met Gly Lys Leu Val Gly Arg Asn Ser Asp Thr
                    125                   130                   135

    Asn Arg Glu Ala Leu Glu Glu Phe Lys Lys Leu Val Gln Arg Lys
                    140                   145                   150

    Gly Leu Ser Glu Glu Asp Ile Phe Thr Pro Leu Gln Thr Gly Ser
                    155                   160                   165

    Cys Val Pro Glu His
                    170

<210> 163
<211> 22
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-22
<223> Synthetic construct.

<400> 163
 ggagatgaag accctgttcc tg 22

<210> 164
<211> 26
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-26
<223> Synthetic construct.

<400> 164
 ggagatgaag accctgttcc tgggtg 26
```

<210> 165
<211> 21
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-21
<223> Synthetic construct.

<400> 165
gtcctccgga aagtccttat c 21

<210> 166
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-25
<223> Synthetic construct.

<400> 166
gcctagtgtt cgggaacgca gcttc 25

<210> 167
<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 167
cagggacctg gtacgtgaag gccatggtgg tcgataagga ctttccggag 50

<210> 168
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 168
ctgtccttca ccctggagga ggaggatatc acagggacct ggtac 45

<210> 169
<211> 1204
<212> DNA
<213> Homo sapiens

<400> 169

```
gttccgcaga tgcagaggtt gaggtggctg cgggactgga agtcatcggg 50

cagaggtctc acagcagcca aggaacctgg ggcccgctcc tcccccctcc 100

aggccatgag gattctgcag ttaatcctgc ttgctctggc aacagggctt 150

gtaggggag agaccaggat catcaagggg ttcgagtgca agcctcactc 200

ccagccctgg caggcagccc tgttcgagaa gacgcggcta ctctgtgggg 250

cgacgctcat cgcccccaga tggctcctga cagcagccca ctgcctcaag 300

ccccgctaca tagttcacct ggggcagcac aacctccaga aggaggaggg 350

ctgtgagcag acccggacag ccactgagtc cttcccccac cccggcttca 400

acaacagcct ccccaacaaa gaccaccgca atgacatcat gctggtgaag 450

atggcatcgc cagtctccat cacctgggct gtgcgacccc tcaccctctc 500

ctcacgctgt gtcactgctg gcaccagctg cctcatttcc ggctggggca 550

gcacgtccag cccccagtta cgcctgcctc acaccttgcg atgcgccaac 600

atcaccatca ttgagcacca gaagtgtgag aacgcctacc ccggcaacat 650

cacagacacc atggtgtgtg ccagcgtgca ggaaggggc aaggactcct 700

gccaggtgta ctccggggc cctctggtct gtaaccagtc tcttcaaggc 750

attatctcct ggggccagga tccgtgtgcg atcacccgaa agcctggtgt 800

ctacacgaaa gtctgcaaat atgtggactg gatccaggag acgatgaaga 850

caattagac tggacccacc caccacagcc catcaccctc catttccact 900

tggtgtttgg ttcctgttca ctctgttaat aagaaaccct aagccaagac 950

cctctacgaa cattctttgg gcctcctgga ctacaggaga tgctgtcact 1000

taataatcaa cctggggttc gaaatcagtg agacctggat tcaaattctg 1050

ccttgaaata ttgtgactct gggaatgaca cacctggtt tgttctctgt 1100

tgtatcccca gccccaaaga cagctcctgg ccatatatca aggtttcaat 1150

aaatatttgc taaatgaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1200

aaaa 1204

<210> 170
<211> 250
<212> PRT
<213> Homo sapiens

<400> 170
Met Arg Ile Leu Gln Leu Ile Leu Leu Ala Leu Ala Thr Gly Leu
 1               5                  10                  15
```

171

```
Val Gly Gly Glu Thr Arg Ile Ile Lys Gly Phe Glu Cys Lys Pro
              20              25              30

His Ser Gln Pro Trp Gln Ala Ala Leu Phe Glu Lys Thr Arg Leu
              35              40              45

Leu Cys Gly Ala Thr Leu Ile Ala Pro Arg Trp Leu Leu Thr Ala
              50              55              60

Ala His Cys Leu Lys Pro Arg Tyr Ile Val His Leu Gly Gln His
              65              70              75

Asn Leu Gln Lys Glu Glu Gly Cys Glu Gln Thr Arg Thr Ala Thr
              80              85              90

Glu Ser Phe Pro His Pro Gly Phe Asn Asn Ser Leu Pro Asn Lys
              95              100             105

Asp His Arg Asn Asp Ile Met Leu Val Lys Met Ala Ser Pro Val
              110             115             120

Ser Ile Thr Trp Ala Val Arg Pro Leu Thr Leu Ser Ser Arg Cys
              125             130             135

Val Thr Ala Gly Thr Ser Cys Leu Ile Ser Gly Trp Gly Ser Thr
              140             145             150

Ser Ser Pro Gln Leu Arg Leu Pro His Thr Leu Arg Cys Ala Asn
              155             160             165

Ile Thr Ile Ile Glu His Gln Lys Cys Glu Asn Ala Tyr Pro Gly
              170             175             180

Asn Ile Thr Asp Thr Met Val Cys Ala Ser Val Gln Glu Gly Gly
              185             190             195

Lys Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Asn
              200             205             210

Gln Ser Leu Gln Gly Ile Ile Ser Trp Gly Gln Asp Pro Cys Ala
              215             220             225

Ile Thr Arg Lys Pro Gly Val Tyr Thr Lys Val Cys Lys Tyr Val
              230             235             240

Asp Trp Ile Gln Glu Thr Met Lys Asn Asn
              245             250
```

<210> 171
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-25
<223> Synthetic construct.

<400> 171
 ggctgcggga ctggaagtca tcggg 25

<210> 172
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 172
 ctccaggcca tgaggattct gcag 24

<210> 173
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 173
 cctctggtct gtaaccag 18

<210> 174
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 174
 tctgtgatgt tgccggggta ggcg 24

<210> 175
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-25
<223> Synthetic construct.

<400> 175
 cgtgtagaca ccaggctttc gggtg 25

<210> 176
<211> 18
<212> DNA

173

<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 176
cccttgatga tcctggtc 18

<210> 177
<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 177
aggccatgag gattctgcag ttaatcctgc ttgctctggc aacagggctt 50

<210> 178
<211> 43
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-43
<223> Synthetic construct.

<400> 178
gagagaccag gatcatcaag gggttcgagt gcaagcctca ctc 43

<210> 179
<211> 907
<212> DNA
<213> Homo sapiens

<400> 179
gagcagtgtt ctgctggagc cgatgccaaa aaccatgcat ttcttattca 50

gattcattgt tttctttttat ctgtggggcc tttttactgc tcagagacaa 100

aagaaagagg agagcaccga agaagtgaaa atagaagttt tgcatcgtcc 150

agaaaactgc tctaagacaa gcaagaaggg agacctacta aatgcccatt 200

atgacggcta cctggctaaa gacggctcga aattctactg cagccggaca 250

caaaatgaag gccacccccaa atggtttgtt cttggtgttg ggcaagtcat 300

aaaaggccta gacattgcta tgacagatat gtgccctgga gaaaagcgaa 350

aagtagttat accccccttca tttgcatacg gaaaggaagg ctatgcagaa 400

174

ggcaagattc caccggatgc tacattgatt tttgagattg aactttatgc 450

tgtgaccaaa ggaccacgga gcattgagac atttaaacaa atagacatgg 500

acaatgacag gcagctctct aaagccgaga taaacctcta cttgcaaagg 550

gaatttgaaa aagatgagaa gccacgtgac aagtcatatc aggatgcagt 600

tttagaagat attttttaaga agaatgacca tgatggtgat ggcttcattt 650

ctcccaagga atacaatgta taccaacacg atgaactata gcatatttgt 700

atttctactt tttttttttta gctatttact gtactttatg tataaaacaa 750

agtcactttt ctccaagttg tatttgctat ttttcccta tgagaagata 800

ttttgatctc cccaatacat tgattttggt ataataaatg tgaggctgtt 850

ttgcaaactt aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 900

aaaaaaa 907

<210> 180
<211> 222
<212> PRT
<213> Homo sapiens

<400> 180

```
Met Pro Lys Thr Met His Phe Leu Phe Arg Phe Ile Val Phe Phe
 1               5                  10                  15

Tyr Leu Trp Gly Leu Phe Thr Ala Gln Arg Gln Lys Lys Glu Glu
                20                  25                  30

Ser Thr Glu Glu Val Lys Ile Glu Val Leu His Arg Pro Glu Asn
                35                  40                  45

Cys Ser Lys Thr Ser Lys Lys Gly Asp Leu Leu Asn Ala His Tyr
                50                  55                  60

Asp Gly Tyr Leu Ala Lys Asp Gly Ser Lys Phe Tyr Cys Ser Arg
                65                  70                  75

Thr Gln Asn Glu Gly His Pro Lys Trp Phe Val Leu Gly Val Gly
                80                  85                  90

Gln Val Ile Lys Gly Leu Asp Ile Ala Met Thr Asp Met Cys Pro
                95                  100                 105

Gly Glu Lys Arg Lys Val Val Ile Pro Pro Ser Phe Ala Tyr Gly
                110                 115                 120

Lys Glu Gly Tyr Ala Glu Gly Lys Ile Pro Pro Asp Ala Thr Leu
                125                 130                 135

Ile Phe Glu Ile Glu Leu Tyr Ala Val Thr Lys Gly Pro Arg Ser
                140                 145                 150
```

175

```
Ile Glu Thr Phe Lys Gln Ile Asp Met Asp Asn Asp Arg Gln Leu
              155             160                 165

Ser Lys Ala Glu Ile Asn Leu Tyr Leu Gln Arg Glu Phe Glu Lys
              170             175                 180

Asp Glu Lys Pro Arg Asp Lys Ser Tyr Gln Asp Ala Val Leu Glu
              185             190                 195

Asp Ile Phe Lys Lys Asn Asp His Asp Gly Asp Gly Phe Ile Ser
              200             205                 210

Pro Lys Glu Tyr Asn Val Tyr Gln His Asp Glu Leu
              215             220
```

<210> 181
<211> 22
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-22
<223> Synthetic construct.

<400> 181
 gtgttctgct ggagccgatg cc 22

<210> 182
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 182
 gacatggaca atgacagg 18

<210> 183
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 183
 cctttcagga tgtaggag 18

<210> 184
<211> 18
<212> DNA
<213> Artificial

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<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 184
  gatgtctgcc accccaag 18

<210> 185
<211> 27
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-27
<223> Synthetic construct.

<400> 185
  gcatcctgat atgacttgtc acgtggc 27

<210> 186
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 186
  tacaagaggg aagaggagtt gcac 24

<210> 187
<211> 52
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-52
<223> Synthetic construct.

<400> 187
  gcccattatg acggctacct ggctaaagac ggctcgaaat tctactgcag 50

  cc 52

<210> 188
<211> 573
<212> DNA
<213> Homo sapiens

<400> 188
  cagaaatgca gggaccattg cttcttccag gcctctgctt tctgctgagc 50

  ctctttggag ctgtgactca gaaaaccaaa acttcctgtg ctaagtgccc 100
```

177

```
cccaaatgct tcctgtgtca ataacactca ctgcacctgc aaccatggat 150

atacttctgg atctgggcag aaactattca cattcccctt ggagacatgt 200

aacgccaggc atggtggctc gcgcctgtaa tcccagttct ttgggaagcc 250

aaggcaggtg gatcacctga ggtcaggagt ttgagaccag cctggccaac 300

atagtgaaac cccgtgtcta ctaaaaatac aaaaatcagc cgggcgtggt 350

ggtgcatgcc tgcaatccca gttactcggg aggctgaggc aggagaatcg 400

cttgaactca ggaggcagaa gttgcagtga acccagatcc tgccattgca 450

ctccagcatg gatgacagag caagactccg tctcaaaaag aaaagatagt 500

ttcttgtttc atttcgcgac tgccctctca gtgtttcctg ggatcccctc 550

ccaaataaag tacttatatt ctc 573
```

<210> 189
<211> 74
<212> PRT
<213> Homo sapiens

<400> 189

```
Met Gln Gly Pro Leu Leu Leu Pro Gly Leu Cys Phe Leu Leu Ser
 1               5                   10                  15

Leu Phe Gly Ala Val Thr Gln Lys Thr Lys Thr Ser Cys Ala Lys
               20                  25                  30

Cys Pro Pro Asn Ala Ser Cys Val Asn Asn Thr His Cys Thr Cys
               35                  40                  45

Asn His Gly Tyr Thr Ser Gly Ser Gly Gln Lys Leu Phe Thr Phe
               50                  55                  60

Pro Leu Glu Thr Cys Asn Ala Arg His Gly Gly Ser Arg Leu
               65                  70
```

<210> 190
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 190
```
agggaccatt gcttcttcca ggcc 24
```

<210> 191
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 191
 cgttacatgt ctccaagggg aatg 24

<210> 192
<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 192
 cctgtgctaa gtgcccccca aatgcttcct gtgtcaataa cactcactgc 50

<210> 193
<211> 1091
<212> DNA
<213> Homo sapiens

<400> 193
 caagcaggtc atccccttgg tgaccttcaa agagaagcag agagggcaga 50

 ggtgggggc acagggaaag ggtgacctct gagattcccc ttttcccca 100

 gactttggaa gtgacccacc atggggctca gcatcttttt gctcctgtgt 150

 gttcttgggc tcagccaggc agccacaccg aagattttca atggcactga 200

 gtgtgggcgt aactcacagc cgtggcaggt ggggctgttt gagggcacca 250

 gcctgcgctg cggggggtgtc cttattgacc acaggtgggt cctcacagcg 300

 gctcactgca gcggcagcag gtactgggtg cgcctggggg aacacagcct 350

 cagccagctc gactggaccg agcagatccg gcacagcggc ttctctgtga 400

 cccatcccgg ctacctggga gcctcgacga gccacgagca cgacctccgg 450

 ctgctgcggc tgcgcctgcc cgtccgcgta accagcagcg ttcaaccct 500

 gccctgccc aatgactgtg caaccgctgg caccgagtgc cacgtctcag 550

 gctggggcat caccaaccac ccacggaacc cattcccgga tctgctccag 600

 tgcctcaacc tctccatcgt ctcccatgcc acctgccatg gtgtgtatcc 650

 cgggagaatc acgagcaaca tggtgtgtgc aggcggcgtc ccggggcagg 700

 atgcctgcca gggtgattct gggggccccc tggtgtgtgg gggagtcctt 750

 caaggtctgg tgtcctgggg gtctgtgggg ccctgtggac aagatggcat 800

```
ccctggagtc tacacctata tttgcaagta tgtggactgg atccggatga 850

tcatgaggaa caactgacct gtttcctcca cctccacccc caccccttaa 900

cttgggtacc cctctggccc tcagagcacc aatatctcct ccatcacttc 950

ccctagctcc actcttgttg gcctgggaac ttcttggaac tttaactcct 1000

gccagccctt ctaagaccca cgagcggggt gagagaagtg tgcaatagtc 1050

tggaataaat ataaatgaag gaggggcaaa aaaaaaaaaa a 1091
```

<210> 194
<211> 248
<212> PRT
<213> Homo sapiens

<400> 194

```
Met Gly Leu Ser Ile Phe Leu Leu Leu Cys Val Leu Gly Leu Ser
  1               5                  10                  15

Gln Ala Ala Thr Pro Lys Ile Phe Asn Gly Thr Glu Cys Gly Arg
               20                  25                  30

Asn Ser Gln Pro Trp Gln Val Gly Leu Phe Glu Gly Thr Ser Leu
               35                  40                  45

Arg Cys Gly Gly Val Leu Ile Asp His Arg Trp Val Leu Thr Ala
               50                  55                  60

Ala His Cys Ser Gly Ser Arg Tyr Trp Val Arg Leu Gly Glu His
               65                  70                  75

Ser Leu Ser Gln Leu Asp Trp Thr Glu Gln Ile Arg His Ser Gly
               80                  85                  90

Phe Ser Val Thr His Pro Gly Tyr Leu Gly Ala Ser Thr Ser His
               95                  100                 105

Glu His Asp Leu Arg Leu Leu Arg Leu Arg Leu Pro Val Arg Val
               110                 115                 120

Thr Ser Ser Val Gln Pro Leu Pro Leu Pro Asn Asp Cys Ala Thr
               125                 130                 135

Ala Gly Thr Glu Cys His Val Ser Gly Trp Gly Ile Thr Asn His
               140                 145                 150

Pro Arg Asn Pro Phe Pro Asp Leu Leu Gln Cys Leu Asn Leu Ser
               155                 160                 165

Ile Val Ser His Ala Thr Cys His Gly Val Tyr Pro Gly Arg Ile
               170                 175                 180

Thr Ser Asn Met Val Cys Ala Gly Gly Val Pro Gly Gln Asp Ala
               185                 190                 195

Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Gly Gly Val Leu
```

180

Gln Gly Leu Val Ser Trp Gly Ser Val Gly Pro Cys Gly Gln Asp
                215   220   225

Gly Ile Pro Gly Val Tyr Thr Tyr Ile Cys Lys Tyr Val Asp Trp
                230   235   240

Ile Arg Met Ile Met Arg Asn Asn
                245

<210> 195
<211> 1485
<212> DNA
<213> Homo sapiens

<400> 195
 gcggccacac gcagctagcc ggagcccgga ccaggcgcct gtgcctcctc 50

 ctcgtccctc gccgcgtccg cgaagcctgg agccggcggg agccccgcgc 100

 tcgccatgtc gggcgagctc agcaacaggt tccaaggagg gaaggcgttc 150

 ggcttgctca agcccggca ggagaggagg ctggccgaga tcaaccggga 200

 gtttctgtgt gaccagaagt acagtgatga agagaacctt ccagaaaagc 250

 tcacagcctt caaagagaag tacatggagt ttgacctgaa caatgaaggc 300

 gagattgacc tgatgtcttt aaagaggatg atggagaagc ttggtgtccc 350

 caagacccac ctggagatga agaagatgat ctcagaggtg acaggagggg 400

 tcagtgacac tatatcctac cgagactttg tgaacatgat gctggggaaa 450

 cggtcggctg tcctcaagtt agtcatgatg tttgaaggaa aagccaacga 500

 gagcagcccc aagccagttg ccccccctcc agagagagac attgctagcc 550

 tgccctgagg accccgcctg gactccccag ccttcccacc ccatacctcc 600

 ctcccgatct tgctgccctt cttgacacac tgtgatctct ctctctctca 650

 tttgtttggt cattgagggt ttgtttgtgt tttcatcaat gtctttgtaa 700

 agcacaaatt atctgcctta aaggggctct gggtcgggga atcctgagcc 750

 ttgggtcccc tccctctctt cttccctcct tccccgctcc ctgtgcagaa 800

 gggctgatat caaaccaaaa actagagggg gcagggccag ggcagggagg 850

 cttccagcct gtgttcccct cacttggagg aaccagcact ctccatcctt 900

 tcagaaagtc tccaagccaa gttcaggctc actgacctgg ctctgacgag 950

 gaccccaggc cactctgaga agaccttgga gtagggacaa ggctgcaggg 1000

 cctctttcgg gtttccttgg acagtgccat ggttccagtg ctctggtgtc 1050

```
acccaggaca cagccactcg gggccccgct gccccagctg atccccactc 1100

attccacacc tcttctcatc ctcagtgatg tgaaggtggg aaggaaagga 1150

gcttggcatt gggagccctt caagaaggta ccagaaggaa ccctccagtc 1200

ctgctctctg gccacacctg tgcaggcagc tgagaggcag cgtgcagccc 1250

tactgtccct tactggggca gcagagggct tcggaggcag aagtgaggcc 1300

tggggtttgg ggggaaaggt cagctcagtg ctgttccacc ttttagggag 1350

gatactgagg ggaccaggat gggagaatga ggagtaaaat gctcacggca 1400

aagtcagcag cactggtaag ccaagactga gaaatacaag gttgcttgtc 1450

tgaccccaat ctgcttgaaa aaaaaaaaaa aaaaa 1485
```

<210> 196
<211> 150
<212> PRT
<213> Homo sapiens

<400> 196

```
Met Ser Gly Glu Leu Ser Asn Arg Phe Gln Gly Gly Lys Ala Phe
 1               5                  10                  15

Gly Leu Leu Lys Ala Arg Gln Glu Arg Arg Leu Ala Glu Ile Asn
                20                  25                  30

Arg Glu Phe Leu Cys Asp Gln Lys Tyr Ser Asp Glu Glu Asn Leu
                35                  40                  45

Pro Glu Lys Leu Thr Ala Phe Lys Glu Lys Tyr Met Glu Phe Asp
                50                  55                  60

Leu Asn Asn Glu Gly Glu Ile Asp Leu Met Ser Leu Lys Arg Met
                65                  70                  75

Met Glu Lys Leu Gly Val Pro Lys Thr His Leu Glu Met Lys Lys
                80                  85                  90

Met Ile Ser Glu Val Thr Gly Gly Val Ser Asp Thr Ile Ser Tyr
                95                  100                 105

Arg Asp Phe Val Asn Met Met Leu Gly Lys Arg Ser Ala Val Leu
                110                 115                 120

Lys Leu Val Met Met Phe Glu Gly Lys Ala Asn Glu Ser Ser Pro
                125                 130                 135

Lys Pro Val Gly Pro Pro Pro Glu Arg Asp Ile Ala Ser Leu Pro
                140                 145                 150
```

<210> 197
<211> 4842
<212> DNA
<213> Homo sapiens

<400> 197

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cgcgctcccc gcgcgcctcc tcgggctcca cgcgtcttgc cccgcagagg  50

cagcctcctc caggagcggg gccctgcaca ccatggcccc cgggtgggca  100

ggggtcggcg ccgccgtgcg cgcccgcctg gcgctggcct tggcgctggc  150

gagcgtcctg agtgggcctc cagccgtcgc ctgccccacc aagtgtacct  200

gctccgctgc cagcgtggac tgccacgggc tgggcctccg cgcggttcct  250

cggggcatcc cccgcaacgc tgagcgcctt gacctggaca gaaataatat  300

caccaggatc accaagatgg acttcgctgg gctcaagaac ctccgagtct  350

tgcatctgga agacaaccag gtcagcgtca tcgagagagg cgccttccag  400

gacctgaagc agctagagcg actgcgcctg aacaagaata agctgcaagt  450

ccttccagaa ttgcttttcc agagcacgcc gaagctcacc agactagatt  500

tgagtgaaaa ccagatccag gggatcccga ggaaggcgtt ccgcggcatc  550

accgatgtga agaacctgca actggacaac aaccacatca gctgcattga  600

agatggagcc ttccgagcgc tgcgcgattt ggagatcctt accctcaaca  650

acaacaacat cagtcgcatc ctggtcacca gcttcaacca catgccgaag  700

atccgaactc tgcgcctcca ctccaaccac ctctactgcg actgccacct  750

ggcctggctc tcggattggc tgcgacagcg acggacagtt ggccagttca  800

cactctgcat ggctcctgtg catttgaggg gcttcaacgt ggcggatgtg  850

cagaagaagg agtacgtgtg cccagccccc cactcggagc ccccatcctg  900

caatgccaac tccatctcct gcccttcgcc ctgcacgtgc agcaataaca  950

tcgtggactg tcgaggaaag ggcttgatgg agattcctgc caacttgccg  1000

gagggcatcg tcgaaatacg cctagaacag aactccatca agccatccc   1050

tgcaggagcc ttcacccagt acaagaaact gaagcgaata gacatcagca  1100

agaatcagat atcggatatt gctccagatg ccttccaggg cctgaaatca  1150

ctcacatcgc tggtcctgta tgggaacaag atcaccgaga ttgccaaggg  1200

actgtttgat gggctggtgt ccctacagct gctcctcctc aatgccaaca  1250

agatcaactg cctgcgggtg aacacgtttc aggacctgca gaacctcaac  1300

ttgctctccc tgtatgacaa caagctgcag accatcagca gggggctctt  1350

cgcccctctg cagtccatcc agacactcca cttagcccaa aacccatttg  1400

tgtgcgactg ccacttgaag tggctggccg actacctcca ggacaacccc  1450
```

183

```
atcgagacaa gcggggcccg ctgcagcagc ccgcgccgac tcgccaacaa 1500

gcgcatcagc cagatcaaga gcaagaagtt ccgctgctca ggctccgagg 1550

attaccgcag caggttcagc agcgagtgct tcatggacct cgtgtgcccc 1600

gagaagtgtc gctgtgaggg cacgattgtg gactgctcca accagaagct 1650

ggtccgcatc ccaagccacc tccctgaata tgtcaccgac ctgcgactga 1700

atgacaatga ggtatctgtt ctggaggcca ctggcatctt caagaagttg 1750

cccaacctgc ggaaaataaa tctgagtaac aataagatca aggaggtgcg 1800

agagggagct ttcgatggag cagccagcgt gcaggagctg atgctgacag 1850

ggaaccagct ggagaccgtg cacgggcgcg tgttccgtgg cctcagtggc 1900

ctcaaaacct tgatgctgag gagtaacttg atcagctgtg tgagtaatga 1950

cacctttgcc ggcctgagtt cggtgagact gctgtccctc tatgacaatc 2000

ggatcaccac catcacccct ggggccttca ccacgcttgt ctccctgtcc 2050

accataaacc tcctgtccaa ccccttcaac tgcaactgcc acctggcctg 2100

gctcggcaag tggttgagga agaggcggat cgtcagtggg aaccctaggt 2150

gccagaagcc attttttcctc aaggagattc ccatccagga tgtggccatc 2200

caggacttca cctgtgatgg caacgaggag agtagctgcc agctgagccc 2250

gcgctgcccg gagcagtgca cctgtatgga gacagtggtg cgatgcagca 2300

acaaggggct ccgcgccctc cccagaggca tgcccaagga tgtgaccgag 2350

ctgtacctgg aaggaaacca cctaacagcc gtgcccagag agctgtccgc 2400

cctccgacac ctgacgctta ttgacctgag caacaacagc atcagcatgc 2450

tgaccaatta caccttcagt aacatgtctc acctctccac tctgatċctg 2500

agctacaacc ggctgaggtg catccccgtc cacgccttca cgggctgcg 2550

gtccctgcga gtgctaaccc tccatggcaa tgacatttcc agcgttcctg 2600

aaggctcctt caacgacctc acatctcttt cccatctggc gctgggaacc 2650

aacccactcc actgtgactg cagtcttcgg tggctgtcgg agtgggtgaa 2700

ggcggggtac aaggagcctg gcatcgcccg ctgcagtagc cctgagccca 2750

tggctgacag gctcctgctc accaccccaa cccaccgctt ccagtgcaaa 2800

gggccagtgg acatcaacat tgtggccaaa tgcaatgcct gcctctccag 2850

cccgtgcaag aataacggga catgcacccca ggaccctgtg gagctgtacc 2900
```

184

```
gctgtgcctg ccccctacagc tacaagggca aggactgcac tgtgcccatc 2950

aacacctgca tccagaaccc ctgtcagcat ggaggcacct gccacctgag 3000

tgacagccac aaggatgggt tcagctgctc ctgccctctg ggctttgagg 3050

ggcagcggtg tgagatcaac ccagatgact gtgaggacaa cgactgcgaa 3100

aacaatgcca cctgcgtgga cgggatcaac aactacgtgt gtatctgtcc 3150

gcctaactac acaggtgagc tatgcgacga ggtgattgac cactgtgtgc 3200

ctgagctgaa cctctgtcag catgaggcca agtgcatccc cctggacaaa 3250

ggattcagct gcgagtgtgt ccctggctac agcgggaagc tctgtgagac 3300

agacaatgat gactgtgtgg cccacaagtg ccgccacggg gcccagtgcg 3350

tggacacaat caatggctac acatgcacct gcccccaggg cttcagtgga 3400

cccttctgtg aacacccccc acccatggtc ctactgcaga ccagcccatg 3450

cgaccagtac gagtgccaga cggggcccca gtgcatcgtg gtgcagcagg 3500

agcccacctg ccgctgccca ccaggcttcg ccggccccag atgcgagaag 3550

ctcatcactg tcaacttcgt gggcaaagac tcctacgtgg aactggcctc 3600

cgccaaggtc cgaccccagg ccaacatctc cctgcaggtg gccactgaca 3650

aggacaacgg catccttctc tacaaaggag acaatgaccc cctggcactg 3700

gagctgtacc agggccacgt gcggctggtc tatgacagcc tgagttcccc 3750

tccaaccaca gtgtacagtg tggagacagt gaatgatggg cagtttcaca 3800

gtgtggagct ggtgacgcta aaccagaccc tgaacctagt agtggacaaa 3850

ggaactccaa agagcctggg gaagctccag aagcagccag cagtgggcat 3900

caacagcccc ctctaccttg gaggcatccc cacctccacc ggcctctccg 3950

ccttgcgcca gggcacggac cggcctctag gcggcttcca cggatgcatc 4000

catgaggtgc gcatcaacaa cgagctgcag gacttcaagg ccctcccacc 4050

acagtccctg ggggtgtcac caggctgcaa gtcctgcacc gtgtgcaagc 4100

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gactctgcca atgcctgctc agccttcaag tgtcaccatg ggcagtgcca 4350
```

185

```
catctcagac caaggggagc cctactgcct gtgccagccc ggctttagcg 4400

gcgagcactg ccaacaagag aatccgtgcc tgggacaagt agtccgagag 4450

gtgatccgcc gccagaaagg ttatgcatca tgtgccacag cctccaaggt 4500

gcccatcatg gaatgtcgtg ggggctgtgg gccccagtgc tgccagccca 4550

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tttgtagaag aggtggagag acacttagag tgcggctgcc tcgcgtgttc 4650

ctaagcccct gcccgcctgc ctgccacctc tcggactcca gcttgatgga 4700

gttgggacag ccatgtggga ccccctggtg attcagcatg aaggaaatga 4750

agctggagag gaaggtaaag aagaagagaa tattaagtat attgtaaaat 4800

aaacaaaaaa tagaacttaa aaaaaaaaaa aaaaaaaaaa aa 4842
```

<210> 198
<211> 1523
<212> PRT
<213> Homo sapiens

<400> 198

```
Met Ala Pro Gly Trp Ala Gly Val Gly Ala Ala Val Arg Ala Arg
  1           5              10                  15

Leu Ala Leu Ala Leu Ala Leu Ala Ser Val Leu Ser Gly Pro Pro
              20              25                  30

Ala Val Ala Cys Pro Thr Lys Cys Thr Cys Ser Ala Ala Ser Val
              35              40                  45

Asp Cys His Gly Leu Gly Leu Arg Ala Val Pro Arg Gly Ile Pro
              50              55                  60

Arg Asn Ala Glu Arg Leu Asp Leu Asp Arg Asn Asn Ile Thr Arg
              65              70                  75

Ile Thr Lys Met Asp Phe Ala Gly Leu Lys Asn Leu Arg Val Leu
              80              85                  90

His Leu Glu Asp Asn Gln Val Ser Val Ile Glu Arg Gly Ala Phe
              95              100                 105

Gln Asp Leu Lys Gln Leu Glu Arg Leu Arg Leu Asn Lys Asn Lys
              110             115                 120

Leu Gln Val Leu Pro Glu Leu Leu Phe Gln Ser Thr Pro Lys Leu
              125             130                 135

Thr Arg Leu Asp Leu Ser Glu Asn Gln Ile Gln Gly Ile Pro Arg
              140             145                 150

Lys Ala Phe Arg Gly Ile Thr Asp Val Lys Asn Leu Gln Leu Asp
              155             160                 165
```

186

```
Asn Asn His Ile Ser Cys Ile Glu Asp Gly Ala Phe Arg Ala Leu
              170             175                 180

Arg Asp Leu Glu Ile Leu Thr Leu Asn Asn Asn Asn Ile Ser Arg
              185             190                 195

Ile Leu Val Thr Ser Phe Asn His Met Pro Lys Ile Arg Thr Leu
              200             205                 210

Arg Leu His Ser Asn His Leu Tyr Cys Asp Cys His Leu Ala Trp
              215             220                 225

Leu Ser Asp Trp Leu Arg Gln Arg Arg Thr Val Gly Gln Phe Thr
              230             235                 240

Leu Cys Met Ala Pro Val His Leu Arg Gly Phe Asn Val Ala Asp
              245             250                 255

Val Gln Lys Lys Glu Tyr Val Cys Pro Ala Pro His Ser Glu Pro
              260             265                 270

Pro Ser Cys Asn Ala Asn Ser Ile Ser Cys Pro Ser Pro Cys Thr
              275             280                 285

Cys Ser Asn Asn Ile Val Asp Cys Arg Gly Lys Gly Leu Met Glu
              290             295                 300

Ile Pro Ala Asn Leu Pro Glu Gly Ile Val Glu Ile Arg Leu Glu
              305             310                 315

Gln Asn Ser Ile Lys Ala Ile Pro Ala Gly Ala Phe Thr Gln Tyr
              320             325                 330

Lys Lys Leu Lys Arg Ile Asp Ile Ser Lys Asn Gln Ile Ser Asp
              335             340                 345

Ile Ala Pro Asp Ala Phe Gln Gly Leu Lys Ser Leu Thr Ser Leu
              350             355                 360

Val Leu Tyr Gly Asn Lys Ile Thr Glu Ile Ala Lys Gly Leu Phe
              365             370                 375

Asp Gly Leu Val Ser Leu Gln Leu Leu Leu Asn Ala Asn Lys
              380             385                 390

Ile Asn Cys Leu Arg Val Asn Thr Phe Gln Asp Leu Gln Asn Leu
              395             400                 405

Asn Leu Leu Ser Leu Tyr Asp Asn Lys Leu Gln Thr Ile Ser Lys
              410             415                 420

Gly Leu Phe Ala Pro Leu Gln Ser Ile Gln Thr Leu His Leu Ala
              425             430                 435

Gln Asn Pro Phe Val Cys Asp Cys His Leu Lys Trp Leu Ala Asp
              440             445                 450

Tyr Leu Gln Asp Asn Pro Ile Glu Thr Ser Gly Ala Arg Cys Ser
```

187

```
                    455                 460                 465
Ser Pro Arg Arg Leu Ala Asn Lys Arg Ile Ser Gln Ile Lys Ser
                470                 475                 480
Lys Lys Phe Arg Cys Ser Gly Ser Glu Asp Tyr Arg Ser Arg Phe
                485                 490                 495
Ser Ser Glu Cys Phe Met Asp Leu Val Cys Pro Glu Lys Cys Arg
                500                 505                 510
Cys Glu Gly Thr Ile Val Asp Cys Ser Asn Gln Lys Leu Val Arg
                515                 520                 525
Ile Pro Ser His Leu Pro Glu Tyr Val Thr Asp Leu Arg Leu Asn
                530                 535                 540
Asp Asn Glu Val Ser Val Leu Glu Ala Thr Gly Ile Phe Lys Lys
                545                 550                 555
Leu Pro Asn Leu Arg Lys Ile Asn Leu Ser Asn Asn Lys Ile Lys
                560                 565                 570
Glu Val Arg Glu Gly Ala Phe Asp Gly Ala Ala Ser Val Gln Glu
                575                 580                 585
Leu Met Leu Thr Gly Asn Gln Leu Glu Thr Val His Gly Arg Val
                590                 595                 600
Phe Arg Gly Leu Ser Gly Leu Lys Thr Leu Met Leu Arg Ser Asn
                605                 610                 615
Leu Ile Ser Cys Val Ser Asn Asp Thr Phe Ala Gly Leu Ser Ser
                620                 625                 630
Val Arg Leu Leu Ser Leu Tyr Asp Asn Arg Ile Thr Thr Ile Thr
                635                 640                 645
Pro Gly Ala Phe Thr Thr Leu Val Ser Leu Ser Thr Ile Asn Leu
                650                 655                 660
Leu Ser Asn Pro Phe Asn Cys Asn Cys His Leu Ala Trp Leu Gly
                665                 670                 675
Lys Trp Leu Arg Lys Arg Arg Ile Val Ser Gly Asn Pro Arg Cys
                680                 685                 690
Gln Lys Pro Phe Phe Leu Lys Glu Ile Pro Ile Gln Asp Val Ala
                695                 700                 705
Ile Gln Asp Phe Thr Cys Asp Gly Asn Glu Glu Ser Ser Cys Gln
                710                 715                 720
Leu Ser Pro Arg Cys Pro Glu Gln Cys Thr Cys Met Glu Thr Val
                725                 730                 735
Val Arg Cys Ser Asn Lys Gly Leu Arg Ala Leu Pro Arg Gly Met
                740                 745                 750

                                   188
```

```
Pro Lys Asp Val Thr Glu Leu Tyr Leu Glu Gly Asn His Leu Thr
             755             760                     765

Ala Val Pro Arg Glu Leu Ser Ala Leu Arg His Leu Thr Leu Ile
             770             775                     780

Asp Leu Ser Asn Asn Ser Ile Ser Met Leu Thr Asn Tyr Thr Phe
             785             790                     795

Ser Asn Met Ser His Leu Ser Thr Leu Ile Leu Ser Tyr Asn Arg
             800             805                     810

Leu Arg Cys Ile Pro Val His Ala Phe Asn Gly Leu Arg Ser Leu
             815             820                     825

Arg Val Leu Thr Leu His Gly Asn Asp Ile Ser Ser Val Pro Glu
             830             835                     840

Gly Ser Phe Asn Asp Leu Thr Ser Leu Ser His Leu Ala Leu Gly
             845             850                     855

Thr Asn Pro Leu His Cys Asp Cys Ser Leu Arg Trp Leu Ser Glu
             860             865                     870

Trp Val Lys Ala Gly Tyr Lys Glu Pro Gly Ile Ala Arg Cys Ser
             875             880                     885

Ser Pro Glu Pro Met Ala Asp Arg Leu Leu Leu Thr Thr Pro Thr
             890             895                     900

His Arg Phe Gln Cys Lys Gly Pro Val Asp Ile Asn Ile Val Ala
             905             910                     915

Lys Cys Asn Ala Cys Leu Ser Ser Pro Cys Lys Asn Asn Gly Thr
             920             925                     930

Cys Thr Gln Asp Pro Val Glu Leu Tyr Arg Cys Ala Cys Pro Tyr
             935             940                     945

Ser Tyr Lys Gly Lys Asp Cys Thr Val Pro Ile Asn Thr Cys Ile
             950             955                     960

Gln Asn Pro Cys Gln His Gly Gly Thr Cys His Leu Ser Asp Ser
             965             970                     975

His Lys Asp Gly Phe Ser Cys Ser Cys Pro Leu Gly Phe Glu Gly
             980             985                     990

Gln Arg Cys Glu Ile Asn Pro Asp Asp Cys Glu Asp Asn Asp Cys
             995             1000                    1005

Glu Asn Asn Ala Thr Cys Val Asp Gly Ile Asn Asn Tyr Val Cys
             1010            1015                    1020

Ile Cys Pro Pro Asn Tyr Thr Gly Glu Leu Cys Asp Glu Val Ile
             1025            1030                    1035

Asp His Cys Val Pro Glu Leu Asn Leu Cys Gln His Glu Ala Lys
```

189

```
              1040                    1045                    1050

Cys Ile Pro Leu Asp Lys Gly Phe Ser Cys Glu Cys Val Pro Gly
              1055                    1060                    1065

Tyr Ser Gly Lys Leu Cys Glu Thr Asp Asn Asp Asp Cys Val Ala
              1070                    1075                    1080

His Lys Cys Arg His Gly Ala Gln Cys Val Asp Thr Ile Asn Gly
              1085                    1090                    1095

Tyr Thr Cys Thr Cys Pro Gln Gly Phe Ser Gly Pro Phe Cys Glu
              1100                    1105                    1110

His Pro Pro Pro Met Val Leu Leu Gln Thr Ser Pro Cys Asp Gln
              1115                    1120                    1125

Tyr Glu Cys Gln Asn Gly Ala Gln Cys Ile Val Val Gln Gln Glu
              1130                    1135                    1140

Pro Thr Cys Arg Cys Pro Pro Gly Phe Ala Gly Pro Arg Cys Glu
              1145                    1150                    1155

Lys Leu Ile Thr Val Asn Phe Val Gly Lys Asp Ser Tyr Val Glu
              1160                    1165                    1170

Leu Ala Ser Ala Lys Val Arg Pro Gln Ala Asn Ile Ser Leu Gln
              1175                    1180                    1185

Val Ala Thr Asp Lys Asp Asn Gly Ile Leu Leu Tyr Lys Gly Asp
              1190                    1195                    1200

Asn Asp Pro Leu Ala Leu Glu Leu Tyr Gln Gly His Val Arg Leu
              1205                    1210                    1215

Val Tyr Asp Ser Leu Ser Ser Pro Pro Thr Thr Val Tyr Ser Val
              1220                    1225                    1230

Glu Thr Val Asn Asp Gly Gln Phe His Ser Val Glu Leu Val Thr
              1235                    1240                    1245

Leu Asn Gln Thr Leu Asn Leu Val Val Asp Lys Gly Thr Pro Lys
              1250                    1255                    1260

Ser Leu Gly Lys Leu Gln Lys Gln Pro Ala Val Gly Ile Asn Ser
              1265                    1270                    1275

Pro Leu Tyr Leu Gly Gly Ile Pro Thr Ser Thr Gly Leu Ser Ala
              1280                    1285                    1290

Leu Arg Gln Gly Thr Asp Arg Pro Leu Gly Gly Phe His Gly Cys
              1295                    1300                    1305

Ile His Glu Val Arg Ile Asn Asn Glu Leu Gln Asp Phe Lys Ala
              1310                    1315                    1320

Leu Pro Pro Gln Ser Leu Gly Val Ser Pro Gly Cys Lys Ser Cys
              1325                    1330                    1335

                             190
```

```
Thr Val Cys Lys His Gly Leu Cys Arg Ser Val Glu Lys Asp Ser
            1340                1345                1350

Val Val Cys Glu Cys Arg Pro Gly Trp Thr Gly Pro Leu Cys Asp
            1355                1360                1365

Gln Glu Ala Arg Asp Pro Cys Leu Gly His Arg Cys His His Gly
            1370                1375                1380

Lys Cys Val Ala Thr Gly Thr Ser Tyr Met Cys Lys Cys Ala Glu
            1385                1390                1395

Gly Tyr Gly Gly Asp Leu Cys Asp Asn Lys Asn Asp Ser Ala Asn
            1400                1405                1410

Ala Cys Ser Ala Phe Lys Cys His His Gly Gln Cys His Ile Ser
            1415                1420                1425

Asp Gln Gly Glu Pro Tyr Cys Leu Cys Gln Pro Gly Phe Ser Gly
            1430                1435                1440

Glu His Cys Gln Gln Glu Asn Pro Cys Leu Gly Gln Val Val Arg
            1445                1450                1455

Glu Val Ile Arg Arg Gln Lys Gly Tyr Ala Ser Cys Ala Thr Ala
            1460                1465                1470

Ser Lys Val Pro Ile Met Glu Cys Arg Gly Gly Cys Gly Pro Gln
            1475                1480                1485

Cys Cys Gln Pro Thr Arg Ser Lys Arg Arg Lys Tyr Val Phe Gln
            1490                1495                1500

Cys Thr Asp Gly Ser Ser Phe Val Glu Glu Val Glu Arg His Leu
            1505                1510                1515

Glu Cys Gly Cys Leu Ala Cys Ser
            1520
```

<210> 199
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 199
 atggagattc ctgccaactt gccg 24

<210> 200
<211> 24
<212> DNA
<213> Artificial

<220>

<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 200
 ttgttggcat tgaggaggag cagc 24

<210> 201
<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 201
 gagggcatcg tcgaaatacg cctagaacag aactccatca aagccatccc 50

<210> 202
<211> 753
<212> DNA
<213> Homo sapiens

<400> 202
 ggatgcagga cgctcccctg agctgcctgt caccgactag gtggagcagt 50

 gtttcttccg cagactcaac tgagaagtca gcctctgggg caggcaccag 100

 gaatctgcct tttcagttct gtctccggca ggctttgagg atgaaggctg 150

 cgggcattct gaccctcatt ggctgcctgg tcacaggcgc cgagtccaaa 200

 atctacactc gttgcaaact ggcaaaaata ttctcgaggg ctggcctgga 250

 caattactgg ggcttcagcc ttggaaactg gatctgcatg gcatattatg 300

 agagcggcta caacaccaca gccccgacgg tcctggatga cggcagcatc 350

 gactatggca tcttccagat caacagcttc gcgtggtgca gacgcggaaa 400

 gctgaaggag aacaaccact gccatgtcgc ctgctcagcc ttgatcactg 450

 atgacctcac agatgcaatt atctgtgcca ggaaaattgt taaagagaca 500

 caaggaatga actattggca aggctggaag aaacattgtg agggcagaga 550

 cctgtccgag tggaaaaaag gctgtgaggt ttcctaaact ggaactggac 600

 ccaggatgct ttgcagcaac gccctaggat ttgcagtgaa tgtccaaatg 650

 cctgtgtcat cttgtcccgt ttcctcccaa tattccttct caaacttgga 700

 gagggaaaat taagctatac ttttaagaaa ataaatattt ccatttaaat 750

 gtc 753

<210> 203
<211> 148
<212> PRT
<213> Homo sapiens

<400> 203

```
Met Lys Ala Ala Gly Ile Leu Thr Leu Ile Gly Cys Leu Val Thr
 1               5                  10                  15

Gly Ala Glu Ser Lys Ile Tyr Thr Arg Cys Lys Leu Ala Lys Ile
                20                  25                  30

Phe Ser Arg Ala Gly Leu Asp Asn Tyr Trp Gly Phe Ser Leu Gly
                35                  40                  45

Asn Trp Ile Cys Met Ala Tyr Tyr Glu Ser Gly Tyr Asn Thr Thr
                50                  55                  60

Ala Pro Thr Val Leu Asp Asp Gly Ser Ile Asp Tyr Gly Ile Phe
                65                  70                  75

Gln Ile Asn Ser Phe Ala Trp Cys Arg Arg Gly Lys Leu Lys Glu
                80                  85                  90

Asn Asn His Cys His Val Ala Cys Ser Ala Leu Ile Thr Asp Asp
                95                 100                 105

Leu Thr Asp Ala Ile Ile Cys Ala Arg Lys Ile Val Lys Glu Thr
               110                 115                 120

Gln Gly Met Asn Tyr Trp Gln Gly Trp Lys Lys His Cys Glu Gly
               125                 130                 135

Arg Asp Leu Ser Glu Trp Lys Lys Gly Cys Glu Val Ser
               140                 145
```

<210> 204
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 204
gcaggctttg aggatgaagg ctgc 24

<210> 205
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 205
ctcattggct gcctggtcac aggc 24

<210> 206
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 206
ccagtcggac aggtctctcc cctc 24

<210> 207
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 207
tcagtgacca aggctgagca ggcg 24

<210> 208
<211> 47
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-47
<223> Synthetic construct.

<400> 208
ctacactcgt tgcaaactgg caaaaatatt ctcgagggct ggcctgg 47

<210> 209
<211> 1648
<212> DNA
<213> Homo sapiens

<400> 209
caggccattt gcatcccact gtccttgtgt tcggagccag gccacaccgt 50

cctcagcagt gtcatgtgtt aaaaacgcca agctgaatat atcatgcccc 100

tattaaaact tgtacatggc tccccattgg tttttggaga aaagttcaag 150

cttttttacct tggtgtctgc ctgtatccca gtgttcaggc tggctagacg 200

gcggaagaag atcctatttt actgtcactt cccagatctg cttctcacca 250

194

```
agagagattc ttttcttaaa cgactataca gggcccccaat tgactggata 300

gaggaataca ccacaggcat ggcagactgc atcttagtca acagccagtt 350

cacagctgct gtttttaagg aaacattcaa gtccctgtct cacatagacc 400

ctgatgtcct ctatccatct ctaaatgtca ccagctttga ctcagttgtt 450

cctgaaaagc tggatgacct agtccccaag gggaaaaaat tcctgctgct 500

ctccatcaac agatacgaaa ggaagaaaaa tctgactttg gcactggaag 550

ccctagtaca gctgcgtgga agattgacat cccaagattg ggagagggtt 600

catctgatcg tggcaggtgg ttatgacgag agagtcctgg agaatgtgga 650

acattatcag gaattgaaga aaatggtcca acagtccgac cttggccagt 700

atgtgacctt cttgaggtct ttctcagaca aacagaaaat ctccctcctc 750

cacagctgca cgtgtgtgct ttacacacca agcaatgagc actttggcat 800

tgtccctctg gaagccatgt acatgcagtg cccagtcatt gctgttaatt 850

cgggtggacc cttggagtcc attgaccaca gtgtcacagg gtttctgtgt 900

gagcctgacc cggtgcactt ctcagaagca atagaaaagt tcatccgtga 950

accttcctta aaagccacca tgggcctggc tggaagagcc agagtgaagg 1000

aaaaattttc ccctgaagca tttacagaac agctctaccg atatgttacc 1050

aaactgctgg tataatcaga ttgttttttaa gatctccatt aatgtcattt 1100

ttatggattg tagacccagt tttgaaacca aaaaagaaac ctagaatcta 1150

atgcagaaga gatctttttaa aaaataaact tgagtcttga atgtgagcca 1200

ctttcctata taccacacct ccctgtccac ttttcagaaa aaccatgtct 1250

tttatgctat aatcattcca aattttgcca gtgttaagtt acaaatgtgg 1300

tgtcattcca tgttcagcag agtattttaa ttatattttc tcgggattat 1350

tgctcttctg tctataaatt ttgaatgata ctgtgcctta attggttttc 1400

atagtttaag tgtgtatcat tatcaaagtt gattaatttg gcttcatagt 1450

ataatgagag cagggctatt gtagttccca gattcaatcc accgaagtgt 1500

tcactgtcat ctgttaggga attttttgttt gtcctgtctt tgcctggatc 1550

catagcgaga gtgctctgta ttttttttaa gataatttgt atttttgcac 1600

actgagatat aataaaaggt gtttatcata aaaaaaaaaa aaaaaaa 1648
```
<210> 210
<211> 323

195

<212> PRT
<213> Homo sapiens

<400> 210
```
Met Pro Leu Leu Lys Leu Val His Gly Ser Pro Leu Val Phe Gly
 1               5                  10                  15

Glu Lys Phe Lys Leu Phe Thr Leu Val Ser Ala Cys Ile Pro Val
               20                  25                  30

Phe Arg Leu Ala Arg Arg Arg Lys Lys Ile Leu Phe Tyr Cys His
               35                  40                  45

Phe Pro Asp Leu Leu Leu Thr Lys Arg Asp Ser Phe Leu Lys Arg
               50                  55                  60

Leu Tyr Arg Ala Pro Ile Asp Trp Ile Glu Glu Tyr Thr Thr Gly
               65                  70                  75

Met Ala Asp Cys Ile Leu Val Asn Ser Gln Phe Thr Ala Ala Val
               80                  85                  90

Phe Lys Glu Thr Phe Lys Ser Leu Ser His Ile Asp Pro Asp Val
               95                  100                 105

Leu Tyr Pro Ser Leu Asn Val Thr Ser Phe Asp Ser Val Val Pro
               110                 115                 120

Glu Lys Leu Asp Asp Leu Val Pro Lys Gly Lys Lys Phe Leu Leu
               125                 130                 135

Leu Ser Ile Asn Arg Tyr Glu Arg Lys Lys Asn Leu Thr Leu Ala
               140                 145                 150

Leu Glu Ala Leu Val Gln Leu Arg Gly Arg Leu Thr Ser Gln Asp
               155                 160                 165

Trp Glu Arg Val His Leu Ile Val Ala Gly Gly Tyr Asp Glu Arg
               170                 175                 180

Val Leu Glu Asn Val Glu His Tyr Gln Glu Leu Lys Lys Met Val
               185                 190                 195

Gln Gln Ser Asp Leu Gly Gln Tyr Val Thr Phe Leu Arg Ser Phe
               200                 205                 210

Ser Asp Lys Gln Lys Ile Ser Leu Leu His Ser Cys Thr Cys Val
               215                 220                 225

Leu Tyr Thr Pro Ser Asn Glu His Phe Gly Ile Val Pro Leu Glu
               230                 235                 240

Ala Met Tyr Met Gln Cys Pro Val Ile Ala Val Asn Ser Gly Gly
               245                 250                 255

Pro Leu Glu Ser Ile Asp His Ser Val Thr Gly Phe Leu Cys Glu
               260                 265                 270
```

196

```
Pro Asp Pro Val His Phe Ser Glu Ala Ile Glu Lys Phe Ile Arg
            275                 280             285

Glu Pro Ser Leu Lys Ala Thr Met Gly Leu Ala Gly Arg Ala Arg
            290                 295             300

Val Lys Glu Lys Phe Ser Pro Glu Ala Phe Thr Glu Gln Leu Tyr
            305                 310             315

Arg Tyr Val Thr Lys Leu Leu Val
            320
```

<210> 211
<211> 1554
<212> DNA
<213> Homo sapiens

<400> 211

```
gactacgccg atccgagacg tggctccctg ggcggcagaa ccatgttgga  50

cttcgcgatc ttcgccgtta ccttcttgct ggcgttggtg ggagccgtgc  100

tctacctcta tccggcttcc agacaagctg caggaattcc agggattact  150

ccaactgaag aaaaagatgg taatcttcca gatattgtga atagtggaag  200

tttgcatgag ttcctggtta atttgcatga gagatatggg cctgtggtct  250

ccttctggtt tggcaggcgc ctcgtggtta gtttgggcac tgttgatgta  300

ctgaagcagc atatcaatcc caataagaca tcggaccctt ttgaaaccat  350

gctgaagtca ttattaaggt atcaatctgg tggtggcagt gtgagtgaaa  400

accacatgag gaaaaaattg tatgaaaatg gtgtgactga ttctctgaag  450

agtaactttg ccctcctcct aaagctttca gaagaattat tagataaatg  500

gctctcctac ccagagaccc agcacgtgcc cctcagccag catatgcttg  550

gttttgctat gaagtctgtt acacagatgg taatgggtag tacatttgaa  600

gatgatcagg aagtcattcg cttccagaag aatcatggca cagtttggtc  650

tgagattgga aaaggctttc tagatgggtc acttgataaa aacatgactc  700

ggaaaaaaca atatgaagat gccctcatgc aactggagtc tgttttaagg  750

aacatcataa aagaacgaaa aggaaggaac ttcagtcaac atattttcat  800

tgactcctta gtacaaggga accttaatga ccaacagatc ctagaagaca  850

gtatgatatt ttctctggcc agttgcataa taactgcaaa attgtgtacc  900

tgggcaatct gttttttaac cacctctgaa gaagttcaaa aaaaattata  950

tgaagagata aaccaagttt ttggaaatgg tcctgttact ccagagaaaa  1000
```

ttgagcagct cagatattgt cagcatgtgc tttgtgaaac tgttcgaact 1050

gccaaactga ctccagtttc tgcccagctt caagatattg aaggaaaaat 1100

tgaccgattt attattccta gagagaccct cgtcctttat gcccttggtg 1150

tggtacttca ggatcctaat acttggccat ctccacacaa gtttgatcca 1200

gatcggtttg atgatgaatt agtaatgaaa acttttttcct cacttggatt 1250

ctcaggcaca caggagtgtc cagagttgag gtttgcatat atggtgacca 1300

cagtacttct tagtgtattg gtgaagagac tgcacctact ttctgtggag 1350

ggacaggtta ttgaaacaaa gtatgaactg gtaacatcat caagggaaga 1400

agcttggatc actgtctcaa agagatatta aaattttata catttaaaat 1450

cattgttaaa ttgattgagg aaaacaacca tttaaaaaaa atctatgttg 1500

aatcctttta taaaccagta tcactttgta atataaacac ctatttgtac 1550

ttaa 1554

<210> 212
<211> 462
<212> PRT
<213> Homo sapiens

<400> 212
Met Leu Asp Phe Ala Ile Phe Ala Val Thr Phe Leu Leu Ala Leu
1   5   10   15

Val Gly Ala Val Leu Tyr Leu Tyr Pro Ala Ser Arg Gln Ala Ala
                20   25   30

Gly Ile Pro Gly Ile Thr Pro Thr Glu Glu Lys Asp Gly Asn Leu
                35   40   45

Pro Asp Ile Val Asn Ser Gly Ser Leu His Glu Phe Leu Val Asn
                50   55   60

Leu His Glu Arg Tyr Gly Pro Val Val Ser Phe Trp Phe Gly Arg
                65   70   75

Arg Leu Val Val Ser Leu Gly Thr Val Asp Val Leu Lys Gln His
                80   85   90

Ile Asn Pro Asn Lys Thr Ser Asp Pro Phe Glu Thr Met Leu Lys
                95   100   105

Ser Leu Leu Arg Tyr Gln Ser Gly Gly Gly Ser Val Ser Glu Asn
                110   115   120

His Met Arg Lys Lys Leu Tyr Glu Asn Gly Val Thr Asp Ser Leu
                125   130   135

Lys Ser Asn Phe Ala Leu Leu Leu Lys Leu Ser Glu Glu Leu Leu

198

```
              140                    145                    150

Asp Lys Trp Leu Ser Tyr Pro Glu Thr Gln His Val Pro Leu Ser
              155                    160                    165

Gln His Met Leu Gly Phe Ala Met Lys Ser Val Thr Gln Met Val
              170                    175                    180

Met Gly Ser Thr Phe Glu Asp Asp Gln Glu Val Ile Arg Phe Gln
              185                    190                    195

Lys Asn His Gly Thr Val Trp Ser Glu Ile Gly Lys Gly Phe Leu
              200                    205                    210

Asp Gly Ser Leu Asp Lys Asn Met Thr Arg Lys Lys Gln Tyr Glu
              215                    220                    225

Asp Ala Leu Met Gln Leu Glu Ser Val Leu Arg Asn Ile Ile Lys
              230                    235                    240

Glu Arg Lys Gly Arg Asn Phe Ser Gln His Ile Phe Ile Asp Ser
              245                    250                    255

Leu Val Gln Gly Asn Leu Asn Asp Gln Gln Ile Leu Glu Asp Ser
              260                    265                    270

Met Ile Phe Ser Leu Ala Ser Cys Ile Ile Thr Ala Lys Leu Cys
              275                    280                    285

Thr Trp Ala Ile Cys Phe Leu Thr Thr Ser Glu Glu Val Gln Lys
              290                    295                    300

Lys Leu Tyr Glu Glu Ile Asn Gln Val Phe Gly Asn Gly Pro Val
              305                    310                    315

Thr Pro Glu Lys Ile Glu Gln Leu Arg Tyr Cys Gln His Val Leu
              320                    325                    330

Cys Glu Thr Val Arg Thr Ala Lys Leu Thr Pro Val Ser Ala Gln
              335                    340                    345

Leu Gln Asp Ile Glu Gly Lys Ile Asp Arg Phe Ile Ile Pro Arg
              350                    355                    360

Glu Thr Leu Val Leu Tyr Ala Leu Gly Val Val Leu Gln Asp Pro
              365                    370                    375

Asn Thr Trp Pro Ser Pro His Lys Phe Asp Pro Asp Arg Phe Asp
              380                    385                    390

Asp Glu Leu Val Met Lys Thr Phe Ser Ser Leu Gly Phe Ser Gly
              395                    400                    405

Thr Gln Glu Cys Pro Glu Leu Arg Phe Ala Tyr Met Val Thr Thr
              410                    415                    420

Val Leu Leu Ser Val Leu Val Lys Arg Leu His Leu Leu Ser Val
              425                    430                    435
```

199

```
Glu Gly Gln Val Ile Glu Thr Lys Tyr Glu Leu Val Thr Ser Ser
        440             445             450

Arg Glu Glu Ala Trp Ile Thr Val Ser Lys Arg Tyr
        455             460
```

<210> 213
<211> 759
<212> DNA
<213> Homo sapiens

<400> 213

```
ctagatttgt cggcttgcgg ggagacttca ggagtcgctg tctctgaact  50

tccagcctca gagaccgccg cccttgtccc cgagggccat gggccgggtc 100

tcagggcttg tgccctctcg cttcctgacg ctcctggcgc atctggtggt 150

cgtcatcacc ttattctggt cccgggacag caacatacag gcctgcctgc 200

ctctcacgtt cacccccgag gagtatgaca agcaggacat tcagctggtg 250

gccgcgctct ctgtcaccct gggcctcttt gcagtggagc tggccggttt 300

cctctcagga gtctccatgt tcaacagcac ccagagcctc atctccattg 350

gggctcactg tagtgcatcc gtggccctgt ccttcttcat attcgagcgt 400

tgggagtgca ctacgtattg gtacattttt gtcttctgca gtgcccttcc 450

agctgtcact gaaatggctt tattcgtcac cgtctttggg ctgaaaaaga 500

aacccttctg attaccttca tgacgggaac ctaaggacga agcctacagg 550

ggcaagggcc gcttcgtatt cctggaagaa ggaaggcata ggcttcggtt 600

ttcccctcgg aaactgcttc tgctggagga tatgtgttgg aataattacg 650

tcttgagtct gggattatcc gcattgtatt tagtgctttg taataaaata 700

tgttttgtag taacattaag acttatatac agttttaggg gacaattaaa 750

aaaaaaaaa 759
```

<210> 214
<211> 140
<212> PRT
<213> Homo sapiens

<400> 214
```
Met Gly Arg Val Ser Gly Leu Val Pro Ser Arg Phe Leu Thr Leu
 1             5              10             15

Leu Ala His Leu Val Val Val Ile Thr Leu Phe Trp Ser Arg Asp
            20             25             30

Ser Asn Ile Gln Ala Cys Leu Pro Leu Thr Phe Thr Pro Glu Glu
            35             40             45
```

```
Tyr Asp Lys Gln Asp Ile Gln Leu Val Ala Ala Leu Ser Val Thr
            50                  55                  60

Leu Gly Leu Phe Ala Val Glu Leu Ala Gly Phe Leu Ser Gly Val
            65                  70                  75

Ser Met Phe Asn Ser Thr Gln Ser Leu Ile Ser Ile Gly Ala His
            80                  85                  90

Cys Ser Ala Ser Val Ala Leu Ser Phe Phe Ile Phe Glu Arg Trp
            95                  100                 105

Glu Cys Thr Thr Tyr Trp Tyr Ile Phe Val Phe Cys Ser Ala Leu
            110                 115                 120

Pro Ala Val Thr Glu Met Ala Leu Phe Val Thr Val Phe Gly Leu
            125                 130                 135

Lys Lys Lys Pro Phe
            140
```

<210> 215
<211> 697
<212> DNA
<213> Homo sapiens

<400> 215
```
 tcccggaccc tgccgccctg ccactatgtc ccgccgctct atgctgcttg  50

 cctgggctct ccccagcctc cttcgactcg gagcggctca ggagacagaa  100

 gacccggcct gctgcagccc catagtgccc cggaacgagt ggaaggccct  150

 ggcatcagag tgcgcccagc acctgagcct gcccttacgc tatgtggtgg  200

 tatcgcacac ggcgggcagc agctgcaaca ccccgcctc gtgccagcag  250

 caggcccgga atgtgcagca ctaccacatg aagacactgg gctggtgcga  300

 cgtgggctac aacttcctga ttggagaaga cgggctcgta tacgagggcc  350

 gtggctggaa cttcacgggt gcccactcag gtcacttatg gaaccccatg  400

 tccattggca tcagcttcat gggcaactac atggatcggg tgcccacacc  450

 ccaggccatc cgggcagccc agggtctact ggcctgcggt gtggctcagg  500

 gagccctgag gtccaactat gtgctcaaag acaccggga tgtgcagcgt  550

 acactctctc caggcaacca gctctaccac ctcatccaga attggccaca  600

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 catggccaaa aaccccactg tctccttctc caataaagat gtagctc  697
```

<210> 216
<211> 196
<212> PRT

201

<213> Homo sapiens

<400> 216
```
Met Ser Arg Arg Ser Met Leu Leu Ala Trp Ala Leu Pro Ser Leu
 1               5                  10                  15

Leu Arg Leu Gly Ala Ala Gln Glu Thr Glu Asp Pro Ala Cys Cys
                20                  25                  30

Ser Pro Ile Val Pro Arg Asn Glu Trp Lys Ala Leu Ala Ser Glu
                35                  40                  45

Cys Ala Gln His Leu Ser Leu Pro Leu Arg Tyr Val Val Val Ser
                50                  55                  60

His Thr Ala Gly Ser Ser Cys Asn Thr Pro Ala Ser Cys Gln Gln
                65                  70                  75

Gln Ala Arg Asn Val Gln His Tyr His Met Lys Thr Leu Gly Trp
                80                  85                  90

Cys Asp Val Gly Tyr Asn Phe Leu Ile Gly Glu Asp Gly Leu Val
                95                  100                 105

Tyr Glu Gly Arg Gly Trp Asn Phe Thr Gly Ala His Ser Gly His
                110                 115                 120

Leu Trp Asn Pro Met Ser Ile Gly Ile Ser Phe Met Gly Asn Tyr
                125                 130                 135

Met Asp Arg Val Pro Thr Pro Gln Ala Ile Arg Ala Ala Gln Gly
                140                 145                 150

Leu Leu Ala Cys Gly Val Ala Gln Gly Ala Leu Arg Ser Asn Tyr
                155                 160                 165

Val Leu Lys Gly His Arg Asp Val Gln Arg Thr Leu Ser Pro Gly
                170                 175                 180

Asn Gln Leu Tyr His Leu Ile Gln Asn Trp Pro His Tyr Arg Ser
                185                 190                 195

Pro
```

<210> 217
<211> 1871
<212> DNA
<213> Homo sapiens

<400> 217
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ctgggacccc gaaaagagaa ggggagagcg aggggacgag agcggaggag 50

gaagatgcaa ctgactcgct gctgcttcgt gttcctggtg cagggtagcc 100

tctatctggt catctgtggc caggatgatg gtcctcccgg ctcagaggac 150

cctgagcgtg atgaccacga gggccagccc cggccccggg tgcctcggaa 200
```

202

```
gcggggccac atctcaccta agtcccgccc catggccaat tccactctcc 250

tagggctgct ggccccgcct ggggaggctt ggggcattct tgggcagccc 300

cccaaccgcc cgaaccacag ccccccaccc tcagccaagg tgaagaaaat 350

ctttggctgg ggcgacttct actccaacat caagacggtg gccctgaacc 400

tgctcgtcac agggaagatt gtggaccatg gcaatgggac cttcagcgtc 450

cacttccaac acaatgccac aggccaggga aacatctcca tcagcctcgt 500

gccccccagt aaagctgtag agttccacca ggaacagcag atcttcatcg 550

aagccaaggc ctccaaaatc ttcaactgcc ggatggagtg ggagaaggta 600

gaacggggcc gccggacctc gctttgcacc cacgacccag ccaagatctg 650

ctcccgagac cacgctcaga gctcagccac ctggagctgc tcccagccct 700

tcaaagtcgt ctgtgtctac atcgccttct acagcacgga ctatcggctg 750

gtccagaagg tgtgcccaga ttacaactac catagtgata ccccctacta 800

cccatctggg tgacccgggg caggccacag aggccaggcc agggctggaa 850

ggacaggcct gcccatgcag gagaccatct ggacaccggg cagggaaggg 900

gttgggcctc aggcagggag gggggtggag acgaggagat gccaagtggg 950

gccagggcca agtctcaagt ggcagagaaa gggtcccaag tgctggtccc 1000

aacctgaagc tgtggagtga ctagatcaca ggagcactgg aggaggagtg 1050

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atggatggct gagagggctt cctaggagcc agtcagcagg gtggggtggg 1300

gccagaggag ctctccagcc ctgcctagtg ggcgccctga gccccttgtc 1350

gtgtgctgag catggcatga ggctgaagtg gcaaccctgg ggtctttgat 1400

gtcttgacag attgaccatc tgtctccagc caggccaccc ctttccaaaa 1450

ttccctcttc tgccagtact ccccctgtac cacccattgc tgatggcaca 1500

cccatcctta agctaagaca ggacgattgt ggtcctccca cactaaggcc 1550

acagcccatc cgcgtgctgt gtgtccctct tccaccccaa cccctgctgg 1600

ctcctctggg agcatccatg tcccggagag gggtccctca acagtcagcc 1650
```

203

tcacctgtca gaccgggggtt ctcccggatc tggatggcgc cgccctctca 1700

gcagcgggca cgggtggggc ggggccgggc cgcagagcat gtgctggatc 1750

tgttctgtgt gtctgtctgt gggtgggggg aggggaggga agtcttgtga 1800

aaccgctgat tgctgacttt tgtgtgaaga atcgtgttct tggagcagga 1850

aataaagctt gccccggggc a 1871

<210> 218
<211> 252
<212> PRT
<213> Homo sapiens

<400> 218
```
Met Gln Leu Thr Arg Cys Cys Phe Val Phe Leu Val Gln Gly Ser
 1               5                  10                  15

Leu Tyr Leu Val Ile Cys Gly Gln Asp Asp Gly Pro Pro Gly Ser
            20                  25                  30

Glu Asp Pro Glu Arg Asp Asp His Glu Gly Gln Pro Arg Pro Arg
            35                  40                  45

Val Pro Arg Lys Arg Gly His Ile Ser Pro Lys Ser Arg Pro Met
            50                  55                  60

Ala Asn Ser Thr Leu Leu Gly Leu Leu Ala Pro Pro Gly Glu Ala
            65                  70                  75

Trp Gly Ile Leu Gly Gln Pro Pro Asn Arg Pro Asn His Ser Pro
            80                  85                  90

Pro Pro Ser Ala Lys Val Lys Lys Ile Phe Gly Trp Gly Asp Phe
            95                  100                 105

Tyr Ser Asn Ile Lys Thr Val Ala Leu Asn Leu Leu Val Thr Gly
            110                 115                 120

Lys Ile Val Asp His Gly Asn Gly Thr Phe Ser Val His Phe Gln
            125                 130                 135

His Asn Ala Thr Gly Gln Gly Asn Ile Ser Ile Ser Leu Val Pro
            140                 145                 150

Pro Ser Lys Ala Val Glu Phe His Gln Glu Gln Gln Ile Phe Ile
            155                 160                 165

Glu Ala Lys Ala Ser Lys Ile Phe Asn Cys Arg Met Glu Trp Glu
            170                 175                 180

Lys Val Glu Arg Gly Arg Arg Thr Ser Leu Cys Thr His Asp Pro
            185                 190                 195

Ala Lys Ile Cys Ser Arg Asp His Ala Gln Ser Ser Ala Thr Trp
            200                 205                 210
```

```
Ser Cys Ser Gln Pro Phe Lys Val Val Cys Val Tyr Ile Ala Phe
              215             220             225

Tyr Ser Thr Asp Tyr Arg Leu Val Gln Lys Val Cys Pro Asp Tyr
              230             235             240

Asn Tyr His Ser Asp Thr Pro Tyr Tyr Pro Ser Gly
              245             250
```

<210> 219
<211> 2065
<212> DNA
<213> Homo sapiens

<400> 219

```
gtgaatgtga gggtttgatg actttcagat gtctaggaac cagagtgggt 50

gcagggggccc caggcagggc tgattcttgg gcggaggaga gtagggtaaa 100

gggttctgca tgagctcctt aaaggacaaa ggtaacagag ccagcgagag 150

agctcgaggg gagactttga cttcaagcca cagaattggt ggaagtgtgc 200

gcgccgccgc cgccgtcgct cctgcagcgc tgtcgaccta gccgctagca 250

tcttcccgag caccgggatc ccggggtagg aggcgacgcg ggcgagcacc 300

agcgccagcc ggctgcggct gcccacacgg ctcaccatgg gctccgggcg 350

ccgggcgctg tccgcggtgc cggccgtgct gctggtcctc acgctgccgg 400

ggctgcccgt ctgggcacag aacgacacgg agcccatcgt gctggagggc 450

aagtgtctgg tggtgtgcga ctcgaacccg gccacggact ccaagggctc 500

ctcttcctcc ccgctgggga tatcggtccg ggcggccaac tccaaggtcg 550

ccttctcggc ggtgcggagc accaaccacg agccatccga gatgagcaac 600

aagacgcgca tcatttactt cgatcagatc ctggtgaatg tgggtaattt 650

tttcacattg gagtctgtct ttgtagcacc aagaaaagga atttacagtt 700

tcagttttca cgtgattaaa gtctaccaga gccaaactat ccaggttaac 750

ttgatgttaa atggaaaacc agtaatatct gcctttgcgg gggacaaaga 800

tgttactcgt gaagctgcca cgaatggtgt cctgctctac ctagataaag 850

aggataaggt ttacctaaaa ctggagaaag gtaatttggt tggaggctgg 900

cagtattcca cgttttctgg ctttctggtg ttccccctat aggattcaat 950

ttctccatga tgttcatcca ggtgagggat gacccactcc tgagttattg 1000

gaagatcatt ttttcatcat tggattgatg tcttttattg gtttctcatg 1050

ggtggatatg gattctaagg attctagcct gtctgaacca atacaaaatt 1100
```

```
tcacagatta tttgtgtgtg tctgtttcag tatatttgga ttgggactct 1150

aagcagataa tacctatgct taaatgtaac agtcaaaagc tgtctgcaag 1200

acttattctg aatttcattt cctgggatta ctgaattagt tacagatgtg 1250

gaattttatt tgtttagttt taaaagactg gcaaccaggt ctaaggatta 1300

gaaaactcta aagttctgac ttcaatcaac ggttagtgtg atactgccaa 1350

agaactgtat actgtgttaa tatattgatt atatttgttt ttattccttt 1400

ggaattagtt tgtttggttc ttgtaaaaaa cttggatttt ttttttcagt 1450

aactggtatt atgttttctc ttaaaataag gtaatgaatg gcttgcccac 1500

aaatttacct tgactacgat atcatcgaca tgacttctct caaaaaaaaa 1550

gaatgcttca tagttgtatt ttaattgtat atgtgaaaga gtcatatttt 1600

ccaagttata ttttctaaga agaagaatag atcataaatc tgacaaggaa 1650

aaagttgctt acccaaaatc taagtgctca atccctgagc ctcagcaaaa 1700

cagctcccct ccgagggaaa tcttatactt tattgctcaa ctttaattaa 1750

aatgattgat ataaccact ttattaaaaa cctaaggttt ttttttttc 1800

cgtagacatg accactttat taactggtgg tgggatgctg ttgtttctaa 1850

ttatacctat ttttcaaggc ttctgttgta tttgaagtat catctggttt 1900

tgccttaact ctttaaattg tatatattta tctgtttagc taatattaaa 1950

ttcaaatatc ccatatctaa atttagtgca atatcttgtc ttttgtatag 2000

gtcatatgaa ttcataaaat tatttatgtc tgttatagaa taaagattaa 2050

tatatgttaa aaaaa 2065
```

<210> 220
<211> 201
<212> PRT
<213> Homo sapiens

<400> 220

```
Met Gly Ser Gly Arg Arg Ala Leu Ser Ala Val Pro Ala Val Leu
 1               5                  10                  15

Leu Val Leu Thr Leu Pro Gly Leu Pro Val Trp Ala Gln Asn Asp
                20                  25                  30

Thr Glu Pro Ile Val Leu Glu Gly Lys Cys Leu Val Val Cys Asp
                35                  40                  45

Ser Asn Pro Ala Thr Asp Ser Lys Gly Ser Ser Ser Pro Leu
                50                  55                  60
```

206

```
Gly Ile Ser Val Arg Ala Ala Asn Ser Lys Val Ala Phe Ser Ala
            65                  70                  75

Val Arg Ser Thr Asn His Glu Pro Ser Glu Met Ser Asn Lys Thr
            80                  85                  90

Arg Ile Ile Tyr Phe Asp Gln Ile Leu Val Asn Val Gly Asn Phe
            95                  100                 105

Phe Thr Leu Glu Ser Val Phe Val Ala Pro Arg Lys Gly Ile Tyr
            110                 115                 120

Ser Phe Ser Phe His Val Ile Lys Val Tyr Gln Ser Gln Thr Ile
            125                 130                 135

Gln Val Asn Leu Met Leu Asn Gly Lys Pro Val Ile Ser Ala Phe
            140                 145                 150

Ala Gly Asp Lys Asp Val Thr Arg Glu Ala Ala Thr Asn Gly Val
            155                 160                 165

Leu Leu Tyr Leu Asp Lys Glu Asp Lys Val Tyr Leu Lys Leu Glu
            170                 175                 180

Lys Gly Asn Leu Val Gly Gly Trp Gln Tyr Ser Thr Phe Ser Gly
            185                 190                 195

Phe Leu Val Phe Pro Leu
            200
```

<210> 221
<211> 20
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-20
<223> Synthetic construct.

<400> 221
 acggctcacc atgggctccg 20

<210> 222
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 222
 aggaagagga gcccttggag tccg 24

<210> 223
<211> 40

<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-40
<223> Synthetic construct.

<400> 223
 cgtgctggag ggcaagtgtc tggtggtgtg cgactcgaac 40

<210> 224
<211> 902
<212> DNA
<213> Homo sapiens

<400> 224
 cggtggccat gactgcggcc gtgttcttcg gctgcgcctt cattgccttc 50

 gggcctgcgc tcgccctta tgtcttcacc atcgccatcg agccgttgcg 100

 tatcatcttc ctcatcgccg gagctttctt ctggttggtg tctctactga 150

 tttcgtccct tgtttggttc atggcaagag tcattattga caacaaagat 200

 ggaccaacac agaaatatct gctgatcttt ggagcgtttg tctctgtcta 250

 tatccaagaa atgttccgat ttgcatatta taaactctta aaaaaagcca 300

 gtgaaggttt gaagagtata aacccaggtg agacagcacc ctctatgcga 350

 ctgctggcct atgtttctgg cttgggcttt ggaatcatga gtggagtatt 400

 ttcctttgtg aataccctat ctgactcctt ggggccaggc acagtgggca 450

 ttcatggaga ttctcctcaa ttcttccttt attcagcttt catgacgctg 500

 gtcattatct tgctgcatgt attctggggc attgtatttt ttgatggctg 550

 tgagaagaaa aagtggggca tcctccttat cgttctcctg acccacctgc 600

 tggtgtcagc ccagaccttc ataagttctt attatggaat aaacctggcg 650

 tcagcattta taatcctggt gctcatgggc acctgggcat tcttagctgc 700

 gggaggcagc tgccgaagcc tgaaactctg cctgctctgc caagacaaga 750

 actttcttct ttacaaccag cgctccagat aacctcaggg aaccagcact 800

 tcccaaaccg cagactacat ctttagagga agcacaactg tgcctttttc 850

 tgaaaatccc tttttctggt ggaattgaga aagaaataaa actatgcaga 900

 ta 902

<210> 225
<211> 257
<212> PRT

208

<213> Homo sapiens

<400> 225

```
Met Thr Ala Ala Val Phe Phe Gly Cys Ala Phe Ile Ala Phe Gly
 1               5                  10                  15

Pro Ala Leu Ala Leu Tyr Val Phe Thr Ile Ala Ile Glu Pro Leu
               20                  25                  30

Arg Ile Ile Phe Leu Ile Ala Gly Ala Phe Phe Trp Leu Val Ser
               35                  40                  45

Leu Leu Ile Ser Ser Leu Val Trp Phe Met Ala Arg Val Ile Ile
               50                  55                  60

Asp Asn Lys Asp Gly Pro Thr Gln Lys Tyr Leu Leu Ile Phe Gly
               65                  70                  75

Ala Phe Val Ser Val Tyr Ile Gln Glu Met Phe Arg Phe Ala Tyr
               80                  85                  90

Tyr Lys Leu Leu Lys Lys Ala Ser Glu Gly Leu Lys Ser Ile Asn
               95                 100                 105

Pro Gly Glu Thr Ala Pro Ser Met Arg Leu Leu Ala Tyr Val Ser
              110                 115                 120

Gly Leu Gly Phe Gly Ile Met Ser Gly Val Phe Ser Phe Val Asn
              125                 130                 135

Thr Leu Ser Asp Ser Leu Gly Pro Gly Thr Val Gly Ile His Gly
              140                 145                 150

Asp Ser Pro Gln Phe Phe Leu Tyr Ser Ala Phe Met Thr Leu Val
              155                 160                 165

Ile Ile Leu Leu His Val Phe Trp Gly Ile Val Phe Phe Asp Gly
              170                 175                 180

Cys Glu Lys Lys Lys Trp Gly Ile Leu Leu Ile Val Leu Leu Thr
              185                 190                 195

His Leu Leu Val Ser Ala Gln Thr Phe Ile Ser Ser Tyr Tyr Gly
              200                 205                 210

Ile Asn Leu Ala Ser Ala Phe Ile Ile Leu Val Leu Met Gly Thr
              215                 220                 225

Trp Ala Phe Leu Ala Ala Gly Gly Ser Cys Arg Ser Leu Lys Leu
              230                 235                 240

Cys Leu Leu Cys Gln Asp Lys Asn Phe Leu Leu Tyr Asn Gln Arg
              245                 250                 255

Ser Arg
```

<210> 226

209

<211> 3939
<212> DNA
<213> Homo sapiens

<400> 226
cggcaaccag ccgccgccac caccgctgcc actgccgccc tgccggggcc 50

atgttcgctc tgggcttgcc cttcttggtg ctcttggtgg cctcggtcga 100

gagccatctg ggggttctgg ggcccaagaa cgtctcgcag aaagacgccg 150

agtttgagcg cacctacgtg gacgaggtca acagcgagct ggtcaacatc 200

tacaccttca accatactgt gacccgcaac aggacagagg gcgtgcgtgt 250

gtctgtgaac gtcctgaaca agcagaaggg ggcgccgttg ctgtttgtgg 300

tccgccagaa ggaggctgtg gtgtccttcc aggtgcccct aatcctgcga 350

gggatgtttc agcgcaagta cctctaccaa aaagtggaac gaaccctgtg 400

tcagcccccc accaagaatg agtcggagat tcagttcttc tacgtggatg 450

tgtccaccct gtcaccagtc aacaccacat accagctccg ggtcagccgc 500

atggacgatt ttgtgctcag gactggggag cagttcagct tcaataccac 550

agcagcacag ccccagtact tcaagtatga gttccctgaa ggcgtggact 600

cggtaattgt caaggtgacc tccaacaagg ccttcccctg ctcagtcatc 650

tccattcagg atgtgctgtg tcctgtctat gacctggaca acaacgtagc 700

cttcatcggc atgtaccaga cgatgaccaa gaaggcggcc atcaccgtac 750

agcgcaaaga cttccccagc aacagctttt atgtggtggt ggtggtgaag 800

accgaagacc aagcctgcgg gggctccctg cctttctacc ccttcgcaga 850

agatgaaccg gtcgatcaag gcaccgccca gaaaaccctg tcagtgctgg 900

tgtctcaagc agtcacgtct gaggcatacg tcagtgggat gctctttgc 950

ctgggtatat ttctctcctt ttacctgctg accgtcctcc tggcctgctg 1000

ggagaactgg aggcagaaga agaagaccct gctggtggcc attgaccgag 1050

cctgcccaga aagcggtcac cctcgagtcc tggctgattc ttttcctggc 1100

agttcccctt atgagggtta caactatggc tcctttgaga atgtttctgg 1150

atctaccgat ggtctggttg acagcgctgg cactggggac ctctcttacg 1200

gttaccaggg ccgctccttt gaacctgtag gtactcggcc ccgagtggac 1250

tccatgagct ctgtggagga ggatgactac gacacattga ccgacatcga 1300

ttccgacaag aatgtcattc gcaccaagca atacctctat gtggctgacc 1350

210

```
tggcacggaa ggacaagcgt gttctgcgga aaaagtacca gatctacttc 1400

tggaacattg ccaccattgc tgtcttctat gcccttcctg tggtgcagct 1450

ggtgatcacc taccagacgg tggtgaatgt cacagggaat caggacatct 1500

gctactacaa cttcctctgc gcccacccac tgggcaatct cagcgccttc 1550

aacaacatcc tcagcaacct ggggtacatc ctgctggggc tgcttttcct 1600

gctcatcatc ctgcaacggg agatcaacca caaccgggcc ctgctgcgca 1650

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acatgatcgc cggactctgc atgctgaagc tctaccagaa gcggcacccg 1850

gacatcaacg ccagcgccta cagtgcctac gcctgcctgg ccattgtcat 1900

cttcttctct gtgctgggcg tggtctttgg caaagggaac acggcgttct 1950

ggatcgtctt ctccatcatt cacatcatcg ccaccctgct cctcagcacg 2000

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gcaggcctgc tcccctggaa cccccagatg ttggccaaat tgctgctttc 2800
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211

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ttctcagtgt tggggccttc catgggcccc tgtcctttgg ctctccattt 2850

gtccctttgc aagaggaagg atggaaggga caccctcccc atttcatgcc 2900

ttgcattttg cccgtcctcc tccccacaat gccccagcct gggacctaag 2950

gcctcttttt cctcccatac tcccactcca gggcctagtc tggggcctga 3000

atctctgtcc tgtatcaggg ccccagttct ctttgggctg tccctggctg 3050

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ggggttggc cagctggtgc cagacttttg gtgctaaggc ctgcaagggg 3150

cctggggcag tgcgtattct cttccctctg acctgtgctc agggctggct 3200

ctttagcaat gcgctcagcc caatttgaga accgccttct gattcaagag 3250

gctgaattca gaggtcacct cttcatccca tcagctccca gactgatgcc 3300

agcaccagga ctggagggag aagcgcctca ccccttccct tccttctttc 3350

caggcccctta gtcttgccaa accccagctg gtggcctttc agtgccattg 3400

acactgccca agaatgtcca ggggcaaagg agggatgata cagagttcag 3450

cccgttctgc ctccacagct gtgggcaccc cagtgcctac cttagaaagg 3500

ggcttcagga agggatgtgc tgtttccctc tacgtgccca gtcctagcct 3550

cgctctagga cccagggctg gcttctaagt ttccgtccag tcttcaggca 3600

agttctgtgt tagtcatgca cacacatacc tatgaaacct tggagtttac 3650

aaagaattgc cccagctctg ggcaccctgg ccaccctggt ccttggatcc 3700

ccttcgtccc acctggtcca ccccagatgc tgaggatggg ggagctcagg 3750

cggggcctct gctttgggga tgggaatgtg ttttttctccc aaacttgttt 3800

ttatagctct gcttgaaggg ctgggagatg aggtgggtct ggatcttttc 3850

tcagagcgtc tccatgctat ggttgcattt ccgttttcta tgaatgaatt 3900

tgcattcaat aaacaaccag actcaaaaaa aaaaaaaaa 3939
```

```
<210> 227
<211> 832
<212> PRT
<213> Homo sapiens

<400> 227
Met Phe Ala Leu Gly Leu Pro Phe Leu Val Leu Leu Val Ala Ser
1               5                   10                  15

Val Glu Ser His Leu Gly Val Leu Gly Pro Lys Asn Val Ser Gln
                20                  25                  30
```

212

```
Lys Asp Ala Glu Phe Glu Arg Thr Tyr Val Asp Glu Val Asn Ser
                35                  40                      45

Glu Leu Val Asn Ile Tyr Thr Phe Asn His Thr Val Thr Arg Asn
                50                  55                      60

Arg Thr Glu Gly Val Arg Val Ser Val Asn Val Leu Asn Lys Gln
                65                  70                      75

Lys Gly Ala Pro Leu Leu Phe Val Val Arg Gln Lys Glu Ala Val
                80                  85                      90

Val Ser Phe Gln Val Pro Leu Ile Leu Arg Gly Met Phe Gln Arg
                95                  100                     105

Lys Tyr Leu Tyr Gln Lys Val Glu Arg Thr Leu Cys Gln Pro Pro
                110                 115                     120

Thr Lys Asn Glu Ser Glu Ile Gln Phe Phe Tyr Val Asp Val Ser
                125                 130                     135

Thr Leu Ser Pro Val Asn Thr Thr Tyr Gln Leu Arg Val Ser Arg
                140                 145                     150

Met Asp Asp Phe Val Leu Arg Thr Gly Glu Gln Phe Ser Phe Asn
                155                 160                     165

Thr Thr Ala Ala Gln Pro Gln Tyr Phe Lys Tyr Glu Phe Pro Glu
                170                 175                     180

Gly Val Asp Ser Val Ile Val Lys Val Thr Ser Asn Lys Ala Phe
                185                 190                     195

Pro Cys Ser Val Ile Ser Ile Gln Asp Val Leu Cys Pro Val Tyr
                200                 205                     210

Asp Leu Asp Asn Asn Val Ala Phe Ile Gly Met Tyr Gln Thr Met
                215                 220                     225

Thr Lys Lys Ala Ala Ile Thr Val Gln Arg Lys Asp Phe Pro Ser
                230                 235                     240

Asn Ser Phe Tyr Val Val Val Val Val Lys Thr Glu Asp Gln Ala
                245                 250                     255

Cys Gly Gly Ser Leu Pro Phe Tyr Pro Phe Ala Glu Asp Glu Pro
                260                 265                     270

Val Asp Gln Gly His Arg Gln Lys Thr Leu Ser Val Leu Val Ser
                275                 280                     285

Gln Ala Val Thr Ser Glu Ala Tyr Val Ser Gly Met Leu Phe Cys
                290                 295                     300

Leu Gly Ile Phe Leu Ser Phe Tyr Leu Leu Thr Val Leu Leu Ala
                305                 310                     315

Cys Trp Glu Asn Trp Arg Gln Lys Lys Lys Thr Leu Leu Val Ala
```

213

                    320   325   330

Ile Asp Arg Ala Cys Pro Glu Ser Gly His Pro Arg Val Leu Ala
                335   340   345

Asp Ser Phe Pro Gly Ser Ser Pro Tyr Glu Gly Tyr Asn Tyr Gly
                350   355   360

Ser Phe Glu Asn Val Ser Gly Ser Thr Asp Gly Leu Val Asp Ser
                365   370   375

Ala Gly Thr Gly Asp Leu Ser Tyr Gly Tyr Gln Gly Arg Ser Phe
                380   385   390

Glu Pro Val Gly Thr Arg Pro Arg Val Asp Ser Met Ser Ser Val
                395   400   405

Glu Glu Asp Asp Tyr Asp Thr Leu Thr Asp Ile Asp Ser Asp Lys
                410   415   420

Asn Val Ile Arg Thr Lys Gln Tyr Leu Tyr Val Ala Asp Leu Ala
                425   430   435

Arg Lys Asp Lys Arg Val Leu Arg Lys Lys Tyr Gln Ile Tyr Phe
                440   445   450

Trp Asn Ile Ala Thr Ile Ala Val Phe Tyr Ala Leu Pro Val Val
                455   460   465

Gln Leu Val Ile Thr Tyr Gln Thr Val Val Asn Val Thr Gly Asn
                470   475   480

Gln Asp Ile Cys Tyr Tyr Asn Phe Leu Cys Ala His Pro Leu Gly
                485   490   495

Asn Leu Ser Ala Phe Asn Asn Ile Leu Ser Asn Leu Gly Tyr Ile
                500   505   510

Leu Leu Gly Leu Leu Phe Leu Leu Ile Ile Leu Gln Arg Glu Ile
                515   520   525

Asn His Asn Arg Ala Leu Leu Arg Asn Asp Leu Cys Ala Leu Glu
                530   535   540

Cys Gly Ile Pro Lys His Phe Gly Leu Phe Tyr Ala Met Gly Thr
                545   550   555

Ala Leu Met Met Glu Gly Leu Leu Ser Ala Cys Tyr His Val Cys
                560   565   570

Pro Asn Tyr Thr Asn Phe Gln Phe Asp Thr Ser Phe Met Tyr Met
                575   580   585

Ile Ala Gly Leu Cys Met Leu Lys Leu Tyr Gln Lys Arg His Pro
                590   595   600

Asp Ile Asn Ala Ser Ala Tyr Ser Ala Tyr Ala Cys Leu Ala Ile
                605   610   615

214

```
Val Ile Phe Phe Ser Val Leu Gly Val Val Phe Gly Lys Gly Asn
                620                 625                 630

Thr Ala Phe Trp Ile Val Phe Ser Ile Ile His Ile Ile Ala Thr
                635                 640                 645

Leu Leu Leu Ser Thr Gln Leu Tyr Tyr Met Gly Arg Trp Lys Leu
                650                 655                 660

Asp Ser Gly Ile Phe Arg Arg Ile Leu His Val Leu Tyr Thr Asp
                665                 670                 675

Cys Ile Arg Gln Cys Ser Gly Pro Leu Tyr Val Asp Arg Met Val
                680                 685                 690

Leu Leu Val Met Gly Asn Val Ile Asn Trp Ser Leu Ala Ala Tyr
                695                 700                 705

Gly Leu Ile Met Arg Pro Asn Asp Phe Ala Ser Tyr Leu Leu Ala
                710                 715                 720

Ile Gly Ile Cys Asn Leu Leu Leu Tyr Phe Ala Phe Tyr Ile Ile
                725                 730                 735

Met Lys Leu Arg Ser Gly Glu Arg Ile Lys Leu Ile Pro Leu Leu
                740                 745                 750

Cys Ile Val Cys Thr Ser Val Val Trp Gly Phe Ala Leu Phe Phe
                755                 760                 765

Phe Phe Gln Gly Leu Ser Thr Trp Gln Lys Thr Pro Ala Glu Ser
                770                 775                 780

Arg Glu His Asn Arg Asp Cys Ile Leu Leu Asp Phe Phe Asp Asp
                785                 790                 795

His Asp Ile Trp His Phe Leu Ser Ser Ile Ala Met Phe Gly Ser
                800                 805                 810

Phe Leu Val Leu Leu Thr Leu Asp Asp Asp Leu Asp Thr Val Gln
                815                 820                 825

Arg Asp Lys Ile Tyr Val Phe
                830
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<210> 228
<211> 2848
<212> DNA
<213> Homo sapiens

<400> 228
 gctcaagtgc ctgccttgc cccacccagc ccagcctggc cagagccccc 50

 tggagaagga gctctcttct tgcttggcag ctggaccaag ggagccagtc 100

 ttgggcgctg gagggcctgt cctgaccatg gtccctgcct ggctgtggct 150

 gctttgtgtc tccgtccccc aggctctccc caaggcccag cctgcagagc 200

```
tgtctgtgga agttccagaa aactatggtg gaaatttccc tttatacctg 250

accaagttgc cgctgccccg tgagggggct gaaggccaga tcgtgctgtc 300

aggggactca ggcaaggcaa ctgagggccc atttgctatg gatccagatt 350

ctggcttcct gctggtgacc agggccctgg accgagagga gcaggcagag 400

taccagctac aggtcaccct ggagatgcag gatggacatg tcttgtgggg 450

tccacagcct gtgcttgtgc acgtgaagga tgagaatgac caggtgcccc 500

atttctctca agccatctac agagctcggc tgagccgggg taccaggcct 550

ggcatcccct tcctcttcct tgaggcttca gaccgggatg agccaggcac 600

agccaactcg gatcttcgat tccacatcct gagccaggct ccagcccagc 650

cttccccaga catgttccag ctggagcctc ggctgggggc tctggccctc 700

agccccaagg ggagcaccag ccttgaccac gccctggaga ggacctacca 750

gctgttggta caggtcaagg acatgggtga ccaggcctca ggccaccagg 800

ccactgccac cgtggaagtc tccatcatag agagcacctg ggtgtcccta 850

gagcctatcc acctggcaga gaatctcaaa gtcctatacc cgcaccacat 900

ggcccaggta cactggagtg ggggtgatgt gcactatcac ctggagagcc 950

atcccccggg acccttcgaa gtgaatgcag agggaaacct ctacgtgacc 1000

agagagctgg acagagaagc ccaggctgag tacctgctcc aggtgcgggc 1050

tcagaattcc catggcgagg actatgcggc ccctctggag ctgcacgtgc 1100

tggtgatgga tgagaatgac aacgtgccta tctgccctcc ccgtgacccc 1150

acagtcagca tccctgagct cagtccacca ggtactgaag tgactagact 1200

gtcagcagag gatgcagatg ccccggctc cccaattcc cacgttgtgt 1250

atcagctcct gagccctgag cctgaggatg gggtagaggg gagagccttc 1300

caggtggacc ccacttcagg cagtgtgacg ctgggggtgc tcccactccg 1350

agcaggccag aacatcctgc ttctggtgct ggccatggac ctggcaggcg 1400

cagagggtgg cttcagcagc acgtgtgaag tcgaagtcgc agtcacagat 1450

atcaatgatc acgcccctga gttcatcact tcccagattg ggcctataag 1500

cctccctgag gatgtggagc ccggactct ggtggccatg ctaacagcca 1550

ttgatgctga cctcgagccc gccttccgcc tcatggattt tgccattgag 1600

agggagaca cagaagggac ttttggcctg gattgggagc cagactctgg 1650
```

216

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gcatgttaga ctcagactct gcaagaacct cagttatgag gcagctccaa 1700

gtcatgaggt ggtggtggtg gtgcagagtg tggcgaagct ggtggggcca 1750

ggcccaggcc ctggagccac cgccacggtg actgtgctag tggagagagt 1800

gatgccaccc cccaagttgg accaggagag ctacgaggcc agtgtcccca 1850

tcagtgcccc agccggctct ttcctgctga ccatccagcc ctccgacccc 1900

atcagccgaa ccctcaggtt ctccctagtc aatgactcag agggctggct 1950

ctgcattgag aaattctccg gggaggtgca caccgcccag tccctgcagg 2000

gcgcccagcc tggggacacc tacacggtgc ttgtggaggc ccaggataca 2050

gccctgactc ttgcccctgt gccctcccaa tacctctgca caccccgcca 2100

agaccatggc ttgatcgtga gtggacccag caaggacccc gatctggcca 2150

gtgggcacgg tccctacagc ttcacccttg gtcccaaccc cacggtgcaa 2200

cgggattggc gcctccagac tctcaatggt tcccatgcct acctcacctt 2250

ggccctgcat tgggtggagc cacgtgaaca cataatcccc gtggtggtca 2300

gccacaatgc ccagatgtgg cagctcctgg ttcgagtgat cgtgtgtcgc 2350

tgcaacgtgg aggggcagtg catgcgcaag gtgggccgca tgaagggcat 2400

gcccacgaag ctgtcggcag tgggcatcct tgtaggcacc ctggtagcaa 2450

taggaatctt cctcatcctc attttcaccc actggaccat gtcaaggaag 2500

aaggacccgg atcaaccagc agacagcgtg cccctgaagg cgactgtctg 2550

aatggcccag gcagctctag ctgggagctt ggcctctggc tccatctgag 2600

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gtagaagccc ctccatctgc cctggggtgg aggcaccatc accatcacca 2700

ggcatgtctg cagagcctgg acaccaactt tatggactgc ccatgggagt 2750

gctccaaatg tcagggtgtt tgcccaataa taaagcccca gagaactggg 2800

ctgggcccta tgggaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaag 2848
```

<210> 229
<211> 807
<212> PRT
<213> Homo sapiens

<400> 229
```
Met Val Pro Ala Trp Leu Trp Leu Leu Cys Val Ser Val Pro Gln
 1               5                  10                  15

Ala Leu Pro Lys Ala Gln Pro Ala Glu Leu Ser Val Glu Val Pro
```

217

                         20   25   30

Glu Asn Tyr Gly Gly Asn Phe Pro Leu Tyr Leu Thr Lys Leu Pro
                 35   40   45

Leu Pro Arg Glu Gly Ala Glu Gly Gln Ile Val Leu Ser Gly Asp
                 50   55   60

Ser Gly Lys Ala Thr Glu Gly Pro Phe Ala Met Asp Pro Asp Ser
                 65   70   75

Gly Phe Leu Leu Val Thr Arg Ala Leu Asp Arg Glu Glu Gln Ala
                 80   85   90

Glu Tyr Gln Leu Gln Val Thr Leu Glu Met Gln Asp Gly His Val
                 95   100   105

Leu Trp Gly Pro Gln Pro Val Leu Val His Val Lys Asp Glu Asn
                110   115   120

Asp Gln Val Pro His Phe Ser Gln Ala Ile Tyr Arg Ala Arg Leu
                125   130   135

Ser Arg Gly Thr Arg Pro Gly Ile Pro Phe Leu Phe Leu Glu Ala
                140   145   150

Ser Asp Arg Asp Glu Pro Gly Thr Ala Asn Ser Asp Leu Arg Phe
                155   160   165

His Ile Leu Ser Gln Ala Pro Ala Gln Pro Ser Pro Asp Met Phe
                170   175   180

Gln Leu Glu Pro Arg Leu Gly Ala Leu Ala Leu Ser Pro Lys Gly
                185   190   195

Ser Thr Ser Leu Asp His Ala Leu Glu Arg Thr Tyr Gln Leu Leu
                200   205   210

Val Gln Val Lys Asp Met Gly Asp Gln Ala Ser Gly His Gln Ala
                215   220   225

Thr Ala Thr Val Glu Val Ser Ile Ile Glu Ser Thr Trp Val Ser
                230   235   240

Leu Glu Pro Ile His Leu Ala Glu Asn Leu Lys Val Leu Tyr Pro
                245   250   255

His His Met Ala Gln Val His Trp Ser Gly Gly Asp Val His Tyr
                260   265   270

His Leu Glu Ser His Pro Pro Gly Pro Phe Glu Val Asn Ala Glu
                275   280   285

Gly Asn Leu Tyr Val Thr Arg Glu Leu Asp Arg Glu Ala Gln Ala
                290   295   300

Glu Tyr Leu Leu Gln Val Arg Ala Gln Asn Ser His Gly Glu Asp
                305   310   315

218

```
Tyr Ala Ala Pro Leu Glu Leu His Val Leu Val Met Asp Glu Asn
             320             325             330

Asp Asn Val Pro Ile Cys Pro Pro Arg Asp Pro Thr Val Ser Ile
             335             340             345

Pro Glu Leu Ser Pro Pro Gly Thr Glu Val Thr Arg Leu Ser Ala
             350             355             360

Glu Asp Ala Asp Ala Pro Gly Ser Pro Asn Ser His Val Val Tyr
             365             370             375

Gln Leu Leu Ser Pro Glu Pro Glu Asp Gly Val Glu Gly Arg Ala
             380             385             390

Phe Gln Val Asp Pro Thr Ser Gly Ser Val Thr Leu Gly Val Leu
             395             400             405

Pro Leu Arg Ala Gly Gln Asn Ile Leu Leu Leu Val Leu Ala Met
             410             415             420

Asp Leu Ala Gly Ala Glu Gly Gly Phe Ser Ser Thr Cys Glu Val
             425             430             435

Glu Val Ala Val Thr Asp Ile Asn Asp His Ala Pro Glu Phe Ile
             440             445             450

Thr Ser Gln Ile Gly Pro Ile Ser Leu Pro Glu Asp Val Glu Pro
             455             460             465

Gly Thr Leu Val Ala Met Leu Thr Ala Ile Asp Ala Asp Leu Glu
             470             475             480

Pro Ala Phe Arg Leu Met Asp Phe Ala Ile Glu Arg Gly Asp Thr
             485             490             495

Glu Gly Thr Phe Gly Leu Asp Trp Glu Pro Asp Ser Gly His Val
             500             505             510

Arg Leu Arg Leu Cys Lys Asn Leu Ser Tyr Glu Ala Ala Pro Ser
             515             520             525

His Glu Val Val Val Val Val Gln Ser Val Ala Lys Leu Val Gly
             530             535             540

Pro Gly Pro Gly Pro Gly Ala Thr Ala Thr Val Thr Val Leu Val
             545             550             555

Glu Arg Val Met Pro Pro Pro Lys Leu Asp Gln Glu Ser Tyr Glu
             560             565             570

Ala Ser Val Pro Ile Ser Ala Pro Ala Gly Ser Phe Leu Leu Thr
             575             580             585

Ile Gln Pro Ser Asp Pro Ile Ser Arg Thr Leu Arg Phe Ser Leu
             590             595             600

Val Asn Asp Ser Glu Gly Trp Leu Cys Ile Glu Lys Phe Ser Gly
```

219

Glu Val His Thr Ala Gln Ser Leu Gln Gly Ala Gln Pro Gly Asp
            620   625   630

Thr Tyr Thr Val Leu Val Glu Ala Gln Asp Thr Ala Leu Thr Leu
            635   640   645

Ala Pro Val Pro Ser Gln Tyr Leu Cys Thr Pro Arg Gln Asp His
            650   655   660

Gly Leu Ile Val Ser Gly Pro Ser Lys Asp Pro Asp Leu Ala Ser
            665   670   675

Gly His Gly Pro Tyr Ser Phe Thr Leu Gly Pro Asn Pro Thr Val
            680   685   690

Gln Arg Asp Trp Arg Leu Gln Thr Leu Asn Gly Ser His Ala Tyr
            695   700   705

Leu Thr Leu Ala Leu His Trp Val Glu Pro Arg Glu His Ile Ile
            710   715   720

Pro Val Val Val Ser His Asn Ala Gln Met Trp Gln Leu Leu Val
            725   730   735

Arg Val Ile Val Cys Arg Cys Asn Val Glu Gly Gln Cys Met Arg
            740   745   750

Lys Val Gly Arg Met Lys Gly Met Pro Thr Lys Leu Ser Ala Val
            755   760   765

Gly Ile Leu Val Gly Thr Leu Val Ala Ile Gly Ile Phe Leu Ile
            770   775   780

Leu Ile Phe Thr His Trp Thr Met Ser Arg Lys Lys Asp Pro Asp
            785   790   795

Gln Pro Ala Asp Ser Val Pro Leu Lys Ala Thr Val
            800   805

<210> 230
<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 230
cgccttaccg cgcagcccga agattcacta tggtgaaaat cgccttcaat 50

<210> 231
<211> 24
<212> DNA
<213> Artificial Seqeunce

<220>
<221> Artificial Sequence
<222> full
<223> Synthetic oligonucleotide probe

<400> 231
cctgagctgt aaccccactc cagg 24

<210> 232
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 232
agagtctgtc ccagctatct tgt 23

<210> 233
<211> 2786
<212> DNA
<213> Homo sapiens

<400> 233
ccggggacat gaggtggata ctgttcattg gggcccttat tgggtccagc 50

atctgtggcc aagaaaaatt ttttggggac caagttttga ggattaatgt 100

cagaaatgga gacgagatca gcaaattgag tcaactagtg aattcaaaca 150

acttgaagct caatttctgg aaatctccct cctccttcaa tcggcctgtg 200

gatgtcctgg tcccatctgt cagtctgcag gcatttaaat ccttcctgag 250

atcccagggc ttagagtacg cagtgacaat tgaggacctg caggcccttt 300

tagacaatga agatgatgaa atgcaacaca atgaagggca agaacggagc 350

agtaataact tcaactacgg ggcttaccat tccctggaag ctatttacca 400

cgagatggac aacattgccg cagactttcc tgacctggcg aggagggtga 450

agattggaca ttcgtttgaa aaccggccga tgtatgtact gaagttcagc 500

actgggaaag gcgtgaggcg gccggccgtt tggctgaatg caggcatcca 550

ttcccgagag tggatctccc aggccactgc aatctggacg gcaaggaaga 600

ttgtatctga ttaccagagg gatccagcta tcacctccat cttggagaaa 650

atggatattt tcttgttgcc tgtggccaat cctgatggat atgtgtatac 700

tcaaactcaa aaccgattat ggaggaagac gcggtcccga aatcctggaa 750

gctcctgcat tggtgctgac ccaaatagaa actggaacgc tagttttgca 800

ggaaagggag ccagcgacaa cccttgctcc gaagtgtacc atggacccca 850

221

cgccaattcg gaagtggagg tgaaatcagt ggtagatttc atccaaaaac 900

atgggaattt caagggcttc atcgacctgc acagctactc gcagctgctg 950

atgtatccat atgggtactc agtcaaaaag gccccagatg ccgaggaact 1000

cgacaaggtg gcgaggcttg cggccaaagc tctggcttct gtgtcgggca 1050

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atttgtaccc acacgtgcac gcactgaggc cattgttaaa ggagctcttt 1350

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aagaactggt tctgccagcc tgctcaattt tggtcctgct gtttttgatg 1500

agccttttgt ctgtttctcc ttccaccctg ctggctgggc ggctgcactc 1550

agcatcaccc cttcctgggt ggcatgtctc tctctacctc atttttagaa 1600

ccaaagaaca tctgagatga ttctctaccc tcatccacat ctagccaagc 1650

cagtgacctt gctctggtgg cactgtggga gacaccactt gtctttaggt 1700

gggtctcaaa gatgatgtag aatttccttt aatttctcgc agtcttcctg 1750

gaaaatattt tcctttgagc agcaaatctt gtagggatat cagtgaaggt 1800

ctctccctcc ctcctctcct gttttttttt tttttgagac agagttttgc 1850

tcttgttgcc caggctggag tgtgatggct cgatcttggc tcaccacaac 1900

ctctgcctcc tgggttcaag caattctcct gcctcagcct cttgagtagc 1950

ttggtttata ggcgcatgcc accatgcctg gctaattttg tgtttttagt 2000

agagacaggg tttctccatg ttggtcaggc tggtctcaaa ctcccaacct 2050

caggtgatct gccctccttg gcctcccaga gtgctgggat tacaggtgtg 2100

agccactgtg ccgggcccgt cccctccttt tttaggcctg aatacaaagt 2150

agaagatcac tttccttcac tgtgctgaga atttctagat actacagttc 2200

ttactcctct cttccctttg ttattcagtg tgaccaggat ggcgggaggg 2250

gatctgtgtc actgtaggta ctgtgcccag gaaggctggg tgaagtgacc 2300

222

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atctaaattg caggatggtg aaattatccc catctgtcct aatgggctta 2350

cctcctcttt gccttttgaa ctcacttcaa agatctaggc ctcatcttac 2400

aggtcctaaa tcactcatct ggcctggata atctcactgc cctggcacat 2450

tcccatttgt gctgtggtgt atcctgtgtt tccttgtcct ggtttgtgtg 2500

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tgttgttgtt ttgttttttgt tttttttgctt ttaccaaaca tgtctgtaaa 2700

tcttaacctc ctgcctagga tttgtacagc atctggtgtg tgcttataag 2750

ccaataaata ttcaatgtga aaaaaaaaaa aaaaaa 2786
```

<210> 234
<211> 421
<212> PRT
<213> Homo sapiens

<400> 234

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Met Arg Trp Ile Leu Phe Ile Gly Ala Leu Ile Gly Ser Ser Ile
  1               5                  10                  15

Cys Gly Gln Glu Lys Phe Phe Gly Asp Gln Val Leu Arg Ile Asn
                 20                  25                  30

Val Arg Asn Gly Asp Glu Ile Ser Lys Leu Ser Gln Leu Val Asn
                 35                  40                  45

Ser Asn Asn Leu Lys Leu Asn Phe Trp Lys Ser Pro Ser Ser Phe
                 50                  55                  60

Asn Arg Pro Val Asp Val Leu Val Pro Ser Val Ser Leu Gln Ala
                 65                  70                  75

Phe Lys Ser Phe Leu Arg Ser Gln Gly Leu Glu Tyr Ala Val Thr
                 80                  85                  90

Ile Glu Asp Leu Gln Ala Leu Leu Asp Asn Glu Asp Asp Glu Met
                 95                  100                 105

Gln His Asn Glu Gly Gln Glu Arg Ser Ser Asn Asn Phe Asn Tyr
                 110                 115                 120

Gly Ala Tyr His Ser Leu Glu Ala Ile Tyr His Glu Met Asp Asn
                 125                 130                 135

Ile Ala Ala Asp Phe Pro Asp Leu Ala Arg Arg Val Lys Ile Gly
                 140                 145                 150

His Ser Phe Glu Asn Arg Pro Met Tyr Val Leu Lys Phe Ser Thr
                 155                 160                 165
```

```
Gly Lys Gly Val Arg Arg Pro Ala Val Trp Leu Asn Ala Gly Ile
            170             175             180

His Ser Arg Glu Trp Ile Ser Gln Ala Thr Ala Ile Trp Thr Ala
            185             190             195

Arg Lys Ile Val Ser Asp Tyr Gln Arg Asp Pro Ala Ile Thr Ser
            200             205             210

Ile Leu Glu Lys Met Asp Ile Phe Leu Leu Pro Val Ala Asn Pro
            215             220             225

Asp Gly Tyr Val Tyr Thr Gln Thr Gln Asn Arg Leu Trp Arg Lys
            230             235             240

Thr Arg Ser Arg Asn Pro Gly Ser Ser Cys Ile Gly Ala Asp Pro
            245             250             255

Asn Arg Asn Trp Asn Ala Ser Phe Ala Gly Lys Gly Ala Ser Asp
            260             265             270

Asn Pro Cys Ser Glu Val Tyr His Gly Pro His Ala Asn Ser Glu
            275             280             285

Val Glu Val Lys Ser Val Val Asp Phe Ile Gln Lys His Gly Asn
            290             295             300

Phe Lys Gly Phe Ile Asp Leu His Ser Tyr Ser Gln Leu Leu Met
            305             310             315

Tyr Pro Tyr Gly Tyr Ser Val Lys Lys Ala Pro Asp Ala Glu Glu
            320             325             330

Leu Asp Lys Val Ala Arg Leu Ala Ala Lys Ala Leu Ala Ser Val
            335             340             345

Ser Gly Thr Glu Tyr Gln Val Gly Pro Thr Cys Thr Thr Val Tyr
            350             355             360

Pro Ala Ser Gly Ser Ser Ile Asp Trp Ala Tyr Asp Asn Gly Ile
            365             370             375

Lys Phe Ala Phe Thr Phe Glu Leu Arg Asp Thr Gly Thr Tyr Gly
            380             385             390

Phe Leu Leu Pro Ala Asn Gln Ile Ile Pro Thr Ala Glu Glu Thr
            395             400             405

Trp Leu Gly Leu Lys Thr Ile Met Glu His Val Arg Asp Asn Leu
            410             415             420

Tyr
```

<210> 235
<211> 1743
<212> DNA
<213> Homo sapiens

224

<400> 235

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tgttccaaaa tggcatctta cctttatgga gtactctttg ctgttggcct 100

ctgtgctcca atctactgtg tgtccccggc caatgccccc agtgcatacc 150

cccgcccttc ctccacaaag agcacccctg cctcacaggt gtattccctc 200

aacaccgact ttgccttccg cctataccgc aggctggttt tggagacccc 250

gagtcagaac atcttcttct cccctgtgag tgtctccact tccctggcca 300

tgctctccct tggggcccac tcagtcacca agacccagat tctccagggc 350

ctgggcttca acctcacaca cacaccagag tctgccatcc accagggctt 400

ccagcacctg gttcactcac tgactgttcc cagcaaagac ctgaccttga 450

agatgggaag tgccctcttc gtcaagaagg agctgcagct gcaggcaaat 500

ttcttgggca atgtcaagag gctgtatgaa gcagaagtct tttctacaga 550

tttctccaac ccctccattg cccaggcgag gatcaacagc catgtgaaaa 600

agaagaccca agggaaggtt gtagacataa tccaaggcct tgaccttctg 650

acggccatgg ttctggtgaa tcacattttc tttaaagcca agtgggagaa 700

gccctttcac cttgaatata caagaaagaa cttcccattc ctggtgggcg 750

agcaggtcac tgtgcaagtc cccatgatgc accagaaaga gcagttcgct 800

tttggggtgg atacagagct gaactgcttt gtgctgcaga tggattacaa 850

gggagatgcc gtggccttct ttgtcctccc tagcaagggc aagatgaggc 900

aactggaaca ggccttgtca gccagaacac tgataaagtg gagccactca 950

ctccagaaaa ggtggataga ggtgttcatc cccagatttt ccatttctgc 1000

ctcctacaat ctggaaacca tcctcccgaa gatgggcatc caaaatgcct 1050

ttgacaaaaa tgctgatttt ctggaattg caaagagaga ctccctgcag 1100

gtttctaaag caacccacaa ggctgtgctg gatgtcagtg aagagggcac 1150

tgaggccaca gcagctacca ccaccaagtt catagtccga tcgaaggatg 1200

gtccctctta cttcactgtc tccttcaata ggaccttcct gatgatgatt 1250

acaaataaag ccacagacgg tattctcttt ctaggaaag tggaaaatcc 1300

cactaaatcc taggtgggaa atggcctgtt aactgatggc acattgctaa 1350

tgcacaagaa ataacaaacc acatccctct ttctgttctg agggtgcatt 1400

tgaccccagt ggagctggat cgctggcag ggatgccact tccaaggctc 1450
```

225

```
aatcaccaaa ccatcaacag ggaccccagt cacaagccaa cacccattaa 1500

ccccagtcag tgccctttтc cacaaattct cccaggtaac tagcttcatg 1550

ggatgttgct gggttaccat atttccattc cttggggctc ccaggaatgg 1600

aaatacgcca acccaggtta ggcacctcta ttgcagaatt acaataacac 1650

attcaataaa actaaaatat gaattcaaaa aaaaaaaaaa aaaaaaaaaa 1700

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 1743
```

<210> 236
<211> 417
<212> PRT
<213> Homo sapiens

<400> 236

```
Met Ala Ser Tyr Leu Tyr Gly Val Leu Phe Ala Val Gly Leu Cys
 1               5                  10                  15

Ala Pro Ile Tyr Cys Val Ser Pro Ala Asn Ala Pro Ser Ala Tyr
                20                  25                  30

Pro Arg Pro Ser Ser Thr Lys Ser Thr Pro Ala Ser Gln Val Tyr
                35                  40                  45

Ser Leu Asn Thr Asp Phe Ala Phe Arg Leu Tyr Arg Arg Leu Val
                50                  55                  60

Leu Glu Thr Pro Ser Gln Asn Ile Phe Phe Ser Pro Val Ser Val
                65                  70                  75

Ser Thr Ser Leu Ala Met Leu Ser Leu Gly Ala His Ser Val Thr
                80                  85                  90

Lys Thr Gln Ile Leu Gln Gly Leu Gly Phe Asn Leu Thr His Thr
                95                  100                 105

Pro Glu Ser Ala Ile His Gln Gly Phe Gln His Leu Val His Ser
                110                 115                 120

Leu Thr Val Pro Ser Lys Asp Leu Thr Leu Lys Met Gly Ser Ala
                125                 130                 135

Leu Phe Val Lys Lys Glu Leu Gln Leu Gln Ala Asn Phe Leu Gly
                140                 145                 150

Asn Val Lys Arg Leu Tyr Glu Ala Glu Val Phe Ser Thr Asp Phe
                155                 160                 165

Ser Asn Pro Ser Ile Ala Gln Ala Arg Ile Asn Ser His Val Lys
                170                 175                 180

Lys Lys Thr Gln Gly Lys Val Val Asp Ile Ile Gln Gly Leu Asp
                185                 190                 195

Leu Leu Thr Ala Met Val Leu Val Asn His Ile Phe Phe Lys Ala
```

226

Lys Trp Glu Lys Pro Phe His Leu Glu Tyr Thr Arg Lys Asn Phe
              215   220   225

Pro Phe Leu Val Gly Glu Gln Val Thr Val Gln Val Pro Met Met
              230   235   240

His Gln Lys Glu Gln Phe Ala Phe Gly Val Asp Thr Glu Leu Asn
              245   250   255

Cys Phe Val Leu Gln Met Asp Tyr Lys Gly Asp Ala Val Ala Phe
              260   265   270

Phe Val Leu Pro Ser Lys Gly Lys Met Arg Gln Leu Glu Gln Ala
              275   280   285

Leu Ser Ala Arg Thr Leu Ile Lys Trp Ser His Ser Leu Gln Lys
              290   295   300

Arg Trp Ile Glu Val Phe Ile Pro Arg Phe Ser Ile Ser Ala Ser
              305   310   315

Tyr Asn Leu Glu Thr Ile Leu Pro Lys Met Gly Ile Gln Asn Ala
              320   325   330

Phe Asp Lys Asn Ala Asp Phe Ser Gly Ile Ala Lys Arg Asp Ser
              335   340   345

Leu Gln Val Ser Lys Ala Thr His Lys Ala Val Leu Asp Val Ser
              350   355   360

Glu Glu Gly Thr Glu Ala Thr Ala Ala Thr Thr Thr Lys Phe Ile
              365   370   375

Val Arg Ser Lys Asp Gly Pro Ser Tyr Phe Thr Val Ser Phe Asn
              380   385   390

Arg Thr Phe Leu Met Met Ile Thr Asn Lys Ala Thr Asp Gly Ile
              395   400   405

Leu Phe Leu Gly Lys Val Glu Asn Pro Thr Lys Ser
              410   415

<210> 237
<211> 23
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-23
<223> Synthetic construct.

<400> 237
 caaccatgca aggacagggc agg 23

<210> 238

<211> 47
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-47
<223> Synthetic construct.

<400> 238
 ctttgctgtt ggcctctgtg ctcccaacca tgcaaggaca gggcagg 47

<210> 239
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 239
 tgactcgggg tctccaaaac cagc 24

<210> 240
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 240
 ggtataggcg gaaggcaaag tcgg 24

<210> 241
<211> 48
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-48
<223> Synthetic construct.

<400> 241
 ggcatcttac ctttatggag tactctttgc tgttggcctc tgtgctcc 48

<210> 242
<211> 2436
<212> DNA
<213> Homo sapiens

<400> 242
 ggctgaccgt gctacattgc ctggaggaag cctaaggaac ccaggcatcc 50

```
agctgcccac gcctgagtcc aagattcttc ccaggaacac aaacgtagga 100

gacccacgct cctggaagca ccagccttta tctcttcacc ttcaagtccc 150

ctttctcaag aatcctctgt tctttgccct ctaaagtctt ggtacatcta 200

ggacccaggc atcttgcttt ccagccacaa agagacagat gaagatgcag 250

aaaggaaatg ttctccttat gtttggtcta ctattgcatt tagaagctgc 300

aacaaattcc aatgagacta gcacctctgc caacactgga tccagtgtga 350

tctccagtgg agccagcaca gccaccaact ctgggtccag tgtgacctcc 400

agtggggtca gcacagccac catctcaggg tccagcgtga cctccaatgg 450

ggtcagcata gtcaccaact ctgagttcca tacaacctcc agtgggatca 500

gcacagccac caactctgag ttcagcacag cgtccagtgg gatcagcata 550

gccaccaact ctgagtccag cacaacctcc agtggggcca gcacagccac 600

caactctgag tccagcacac cctccagtgg ggccagcaca gtcaccaact 650

ctgggtccag tgtgacctcc agtggagcca gcactgccac caactctgag 700

tccagcacag tgtccagtag ggccagcact gccaccaact ctgagtctag 750

cacactctcc agtggggcca gcacagccac caactctgac tccagcacaa 800

cctccagtgg ggctagcaca gccaccaact ctgagtccag cacaacctcc 850

agtggggcca gcacagccac caactctgag tccagcacag tgtccagtag 900

ggccagcact gccaccaact ctgagtccag cacaacctcc agtggggcca 950

gcacagccac caactctgag tccagaacga cctccaatgg ggctggcaca 1000

gccaccaact ctgagtccag cacgacctcc agtggggcca gcacagccac 1050

caactctgac tccagcacag tgtccagtgg ggccagcact gccaccaact 1100

ctgagtccag cacgacctcc agtggggcca gcacagccac caactctgag 1150

tccagcacga cctccagtgg ggctagcaca gccaccaact ctgactccag 1200

cacaacctcc agtggggccg gcacagccac caactctgag tccagcacag 1250

tgtccagtgg gatcagcaca gtcaccaatt ctgagtccag cacaccctcc 1300

agtggggcca acacagccac caactctgag tccagtacga cctccagtgg 1350

ggccaacaca gccaccaact ctgagtccag cacagtgtcc agtggggcca 1400

gcactgccac caactctgag tccagcacaa cctccagtgg ggtcagcaca 1450

gccaccaact ctgagtccag cacaacctcc agtggggcta gcacagccac 1500
```

229

```
caactctgac tccagcacaa cctccagtga ggccagcaca gccaccaact 1550

ctgagtctag cacagtgtcc agtgggatca gcacagtcac caattctgag 1600

tccagcacaa cctccagtgg ggccaacaca gccaccaact ctgggtccag 1650

tgtgacctct gcaggctctg aacagcagc tctgactgga atgcacacaa 1700

cttcccatag tgcatctact gcagtgagtg aggcaaagcc tggtgggtcc 1750

ctggtgccgt gggaaatctt cctcatcacc ctggtctcgg ttgtggcggc 1800

cgtggggctc tttgctgggc tcttcttctg tgtgagaaac agcctgtccc 1850

tgagaaacac ctttaacaca gctgtctacc accctcatgg cctcaaccat 1900

ggccttggtc caggccctgg agggaatcat ggagccccc acaggcccag 1950

gtggagtcct aactggttct ggaggagacc agtatcatcg atagccatgg 2000

agatgagcgg gaggaacagc gggccctgag cagccccgga agcaagtgcc 2050

gcattcttca ggaaggaaga gacctgggca cccaagacct ggtttccttt 2100

cattcatccc aggagacccc tcccagcttt gtttgagatc ctgaaaatct 2150

tgaagaaggt attcctcacc tttcttgcct ttaccagaca ctggaaagag 2200

aatactatat tgctcattta gctaagaaat aaatacatct catctaacac 2250

acacgacaaa gagaagctgt gcttgccccg gggtgggtat ctagctctga 2300

gatgaactca gttataggag aaaacctcca tgctggactc catctggcat 2350

tcaaaatctc cacagtaaaa tccaaagacc tcaaaaaaaa aaaaaaaaaa 2400

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 2436
```

<210> 243
<211> 596
<212> PRT
<213> Homo sapiens

<400> 243

```
Met Lys Met Gln Lys Gly Asn Val Leu Leu Met Phe Gly Leu Leu
 1               5                  10                  15

Leu His Leu Glu Ala Ala Thr Asn Ser Asn Glu Thr Ser Thr Ser
                20                  25                  30

Ala Asn Thr Gly Ser Ser Val Ile Ser Ser Gly Ala Ser Thr Ala
                    35                  40                  45

Thr Asn Ser Gly Ser Ser Val Thr Ser Ser Gly Val Ser Thr Ala
                    50                  55                  60

Thr Ile Ser Gly Ser Ser Val Thr Ser Asn Gly Val Ser Ile Val
                    65                  70                  75
```

230

```
Thr Asn Ser Glu Phe His Thr Thr Ser Ser Gly Ile Ser Thr Ala
              80              85                      90

Thr Asn Ser Glu Phe Ser Thr Ala Ser Ser Gly Ile Ser Ile Ala
              95             100                     105

Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala
             110             115                     120

Thr Asn Ser Glu Ser Ser Thr Pro Ser Ser Gly Ala Ser Thr Val
             125             130                     135

Thr Asn Ser Gly Ser Ser Val Thr Ser Ser Gly Ala Ser Thr Ala
             140             145                     150

Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Arg Ala Ser Thr Ala
             155             160                     165

Thr Asn Ser Glu Ser Ser Thr Leu Ser Ser Gly Ala Ser Thr Ala
             170             175                     180

Thr Asn Ser Asp Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala
             185             190                     195

Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala
             200             205                     210

Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Arg Ala Ser Thr Ala
             215             220                     225

Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala
             230             235                     240

Thr Asn Ser Glu Ser Arg Thr Thr Ser Asn Gly Ala Gly Thr Ala
             245             250                     255

Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala
             260             265                     270

Thr Asn Ser Asp Ser Ser Thr Val Ser Ser Gly Ala Ser Thr Ala
             275             280                     285

Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala
             290             295                     300

Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala
             305             310                     315

Thr Asn Ser Asp Ser Ser Thr Thr Ser Ser Gly Ala Gly Thr Ala
             320             325                     330

Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Gly Ile Ser Thr Val
             335             340                     345

Thr Asn Ser Glu Ser Ser Thr Pro Ser Ser Gly Ala Asn Thr Ala
             350             355                     360

Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Asn Thr Ala
```

231

                    365   370   375

Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Gly Ala Ser Thr Ala
            380   385   390

Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Val Ser Thr Ala
            395   400   405

Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala
            410   415   420

Thr Asn Ser Asp Ser Ser Thr Thr Ser Ser Glu Ala Ser Thr Ala
            425   430   435

Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Gly Ile Ser Thr Val
            440   445   450

Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Asn Thr Ala
            455   460   465

Thr Asn Ser Gly Ser Ser Val Thr Ser Ala Gly Ser Gly Thr Ala
            470   475   480

Ala Leu Thr Gly Met His Thr Thr Ser His Ser Ala Ser Thr Ala
            485   490   495

Val Ser Glu Ala Lys Pro Gly Gly Ser Leu Val Pro Trp Glu Ile
            500   505   510

Phe Leu Ile Thr Leu Val Ser Val Val Ala Ala Val Gly Leu Phe
            515   520   525

Ala Gly Leu Phe Phe Cys Val Arg Asn Ser Leu Ser Leu Arg Asn
            530   535   540

Thr Phe Asn Thr Ala Val Tyr His Pro His Gly Leu Asn His Gly
            545   550   555

Leu Gly Pro Gly Pro Gly Gly Asn His Gly Ala Pro His Arg Pro
            560   565   570

Arg Trp Ser Pro Asn Trp Phe Trp Arg Arg Pro Val Ser Ser Ile
            575   580   585

Ala Met Glu Met Ser Gly Arg Asn Ser Gly Pro
            590   595

<210> 244
<211> 26
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-26
<223> Synthetic construct.

<400> 244

```
gaagcaccag cctttatctc ttcacc 26
```

<210> 245
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic sequence.

<400> 245
```
gtcagagttg gtggctgtgc tagc 24
```

<210> 246
<211> 48
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-48
<223> Synthetic construct.

<400> 246
```
ggacccaggc atcttgcttt ccagccacaa agagacagat gaagatgc 48
```

<210> 247
<211> 957
<212> DNA
<213> Homo sapiens

<400> 247
```
gggagagagg ataaatagca gcgtggcttc cctggctcct ctctgcatcc 50

ttcccgacct tcccagcaat atgcatcttg cacgtctggt cggctcctgc 100

tccctccttc tgctactggg ggccctgtct ggatgggcgg ccagcgatga 150

ccccattgag aaggtcattg aagggatcaa ccgagggctg agcaatgcag 200

agagagaggt gggcaaggcc ctggatggca tcaacagtgg aatcacgcat 250

gccggaaggg aagtggagaa ggttttcaac ggacttagca acatggggag 300

ccacaccggc aaggagttgg acaaaggcgt ccaggggctc aaccacggca 350

tggacaaggt tgcccatgag atcaaccatg gtattggaca agcaggaaag 400

gaagcagaga agcttggcca tggggtcaac aacgctgctg gacaggccgg 450

gaaggaagca gacaaagcgg tccaagggtt ccacactggg gtccaccagg 500

ctgggaagga agcagagaaa cttggccaag gggtcaacca tgctgctgac 550

caggctggaa aggaagtgga gaagcttggc caaggtgccc accatgctgc 600
```

233

tggccaggcc gggaaggagc tgcagaatgc tcataatggg gtcaaccaag 650

ccagcaagga ggccaaccag ctgctgaatg caaccatca aagcggatct 700

tccagccatc aaggaggggc cacaaccacg ccgttagcct ctggggcctc 750

agtcaacacg cctttcatca accttccgc cctgtggagg agcgtcgcca 800

acatcatgcc ctaaactggc atccggcctt gctgggagaa taatgtcgcc 850

gttgtcacat cagctgacat gacctggagg ggttgggggt gggggacagg 900

tttctgaaat ccctgaaggg ggttgtactg ggatttgtga ataaacttga 950

tacacca 957

<210> 248
<211> 247
<212> PRT
<213> Homo sapiens

<400> 248
Met His Leu Ala Arg Leu Val Gly Ser Cys Ser Leu Leu Leu Leu
 1   5   10   15

Leu Gly Ala Leu Ser Gly Trp Ala Ala Ser Asp Asp Pro Ile Glu
                20   25   30

Lys Val Ile Glu Gly Ile Asn Arg Gly Leu Ser Asn Ala Glu Arg
                35   40   45

Glu Val Gly Lys Ala Leu Asp Gly Ile Asn Ser Gly Ile Thr His
                50   55   60

Ala Gly Arg Glu Val Glu Lys Val Phe Asn Gly Leu Ser Asn Met
                65   70   75

Gly Ser His Thr Gly Lys Glu Leu Asp Lys Gly Val Gln Gly Leu
                80   85   90

Asn His Gly Met Asp Lys Val Ala His Glu Ile Asn His Gly Ile
                95   100   105

Gly Gln Ala Gly Lys Glu Ala Glu Lys Leu Gly His Gly Val Asn
                110   115   120

Asn Ala Ala Gly Gln Ala Gly Lys Glu Ala Asp Lys Ala Val Gln
                125   130   135

Gly Phe His Thr Gly Val His Gln Ala Gly Lys Glu Ala Glu Lys
                140   145   150

Leu Gly Gln Gly Val Asn His Ala Ala Asp Gln Ala Gly Lys Glu
                155   160   165

Val Glu Lys Leu Gly Gln Gly Ala His His Ala Ala Gly Gln Ala
                170   175   180

234

```
Gly Lys Glu Leu Gln Asn Ala His Asn Gly Val Asn Gln Ala Ser
            185                 190                 195

Lys Glu Ala Asn Gln Leu Leu Asn Gly Asn His Gln Ser Gly Ser
            200                 205                 210

Ser Ser His Gln Gly Gly Ala Thr Thr Thr Pro Leu Ala Ser Gly
            215                 220                 225

Ala Ser Val Asn Thr Pro Phe Ile Asn Leu Pro Ala Leu Trp Arg
            230                 235                 240

Ser Val Ala Asn Ile Met Pro
                245
```

<210> 249
<211> 23
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-23
<223> Synthetic construct.

<400> 249
 caatatgcat cttgcacgtc tgg 23

<210> 250
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 250
 aagcttctct gcttcctttc ctgc 24

<210> 251
<211> 43
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-43
<223> Synthetic construct.

<400> 251
 tgaccccatt gagaaggtca ttgaagggat caaccgaggg ctg 43

<210> 252
<211> 3781
<212> DNA
<213> Homo sapiens

<400> 252

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ctccgggtcc ccaggggctg cgccgggccg gcctggcaag ggggacgagt 50

cagtggacac tccaggaaga gcggccccgc gggggcgat gaccgtgcgc 100

tgaccctgac tcactccagg tccggaggcg ggggcccccg gggcgactcg 150

ggggcggacc gcggggcgga gctgccgccc gtgagtccgg ccgagccacc 200

tgagcccgag ccgcgggaca ccgtcgctcc tgctctccga atgctgcgca 250

ccgcgatggg cctgaggagc tggctcgccg ccccatgggg cgcgctgccg 300

cctcggccac cgctgctgct gctcctgctg ctgctgctcc tgctgcagcc 350

gccgcctccg acctgggcgc tcagcccccg gatcagcctg cctctgggct 400

ctgaagagcg gccattcctc agattcgaag ctgaacacat ctccaactac 450

acagcccttc tgctgagcag ggatggcagg accctgtacg tgggtgctcg 500

agaggccctc tttgcactca gtagcaacct cagcttcctg ccaggcgggg 550

agtaccagga gctgctttgg ggtgcagacg cagagaagaa acagcagtgc 600

agcttcaagg gcaaggaccc acagcgcgac tgtcaaaact acatcaagat 650

cctcctgccg ctcagcggca gtcacctgtt cacctgtggc acagcagcct 700

tcagccccat gtgtacctac atcaacatgg agaacttcac cctggcaagg 750

gacgagaagc ggaatgtcct cctggaagat ggcaagggcc gttgtccctt 800

cgacccgaat ttcaagtcca ctgccctggt ggttgatggc gagctctaca 850

ctggaacagt cagcagcttc caagggaatg acccggccat ctcgcggagc 900

caaagccttc gccccaccaa gaccgagagc tccctcaact ggctgcaaga 950

cccagctttt gtggcctcag cctacattcc tgagagcctg ggcagcttgc 1000

aaggcgatga tgacaagatc tacttttttct tcagcgagac tggccaggaa 1050

tttgagttct ttgagaacac cattgtgtcc cgcattgccc gcatctgcaa 1100

gggcgatgag ggtggagagc gggtgctaca gcagcgctgg acctccttcc 1150

tcaaggccca gctgctgtgc tcacggcccg acgatggctt ccccttcaac 1200

gtgctgcagg atgtcttcac gctgagcccc agcccccagg actggcgtga 1250

cacccttttc tatggggtct tcacttccca gtggcacagg ggaactacag 1300

aaggctctgc cgtctgtgtc ttcacaatga aggatgtgca gagagtcttc 1350

agcggcctct acaaggaggt gaaccgtgag acacagcagt ggtacaccgt 1400

gacccacccg gtgcccacac cccggcctgg agcgtgcatc accaacagtg 1450
```

236

```
cccgggaaag gaagatcaac tcatccctgc agctcccaga ccgcgtgctg 1500

aacttcctca aggaccactt cctgatggac gggcaggtcc gaagccgcat 1550

gctgctgctg cagccccagg ctcgctacca gcgcgtggct gtacaccgcg 1600

tccctggcct gcaccacacc tacgatgtcc tcttcctggg cactggtgac 1650

ggccggctcc acaaggcagt gagcgtgggc ccccgggtgc acatcattga 1700

ggagctgcag atcttctcat cgggacagcc cgtgcagaat ctgctcctgg 1750

acacccacag ggggctgctg tatgcggcct cacactcggg cgtagtccag 1800

gtgcccatgg ccaactgcag cctgtaccgg agctgtgggg actgcctcct 1850

cgcccgggac ccctactgtg cttggagcgg ctccagctgc aagcacgtca 1900

gcctctacca gcctcagctg gccaccaggc cgtggatcca ggacatcgag 1950

ggagccagcg ccaaggacct ttgcagcgcg tcttcggttg tgtccccgtc 2000

ttttgtacca acaggggaga agccatgtga gcaagtccag ttccagccca 2050

acacagtgaa cactttggcc tgcccgctcc tctccaacct ggcgacccga 2100

ctctggctac gcaacggggc ccccgtcaat gcctcggcct cctgccacgt 2150

gctacccact ggggacctgc tgctggtggg cacccaacag ctggggggagt 2200

tccagtgctg gtcactagag gagggcttcc agcagctggt agccagctac 2250

tgcccagagg tggtggagga cggggtggca gaccaaacag atgagggtgg 2300

cagtgtaccc gtcattatca gcacatcgcg tgtgagtgca ccagctggtg 2350

gcaaggccag ctggggtgca gacaggtcct actggaagga gttcctggtg 2400

atgtgcacgc tctttgtgct ggccgtgctg ctcccagttt tattcttgct 2450

ctaccggcac cggaacagca tgaaagtctt cctgaagcag ggggaatgtg 2500

ccagcgtgca ccccaagacc tgccctgtgg tgctgccccc tgagacccgc 2550

ccactcaacg gcctagggcc ccctagcacc ccgctcgatc accgagggta 2600

ccagtccctg tcagacagcc ccccggggggc ccgagtcttc actgagtcag 2650

agaagaggcc actcagcatc caagacagct tcgtggaggt atccccagtg 2700

tgcccccggc cccgggtccg ccttggctcg gagatccgtg actctgtggt 2750

gtgagagctg acttccagag gacgctgccc tggcttcagg ggctgtgaat 2800

gctcggagag ggtcaactgg acctcccctc cgctctgctc ttcgtggaac 2850

acgaccgtgg tgcccggccc ttgggagcct ggagccagc tggcctgctg 2900
```

237

ctctccagtc aagtagcgaa gctcctacca cccagacacc caaacagccg 2950

tggccccaga ggtcctggcc aaatatgggg gcctgcctag gttggtggaa 3000

cagtgctcct tatgtaaact gagccctttg tttaaaaaac aattccaaat 3050

gtgaaactag aatgagaggg aagagatagc atggcatgca gcacacacgg 3100

ctgctccagt tcatggcctc ccaggggtgc tggggatgca tccaaagtgg 3150

ttgtctgaga cagagttgga aaccctcacc aactggcctc ttcaccttcc 3200

acattatccc gctgccaccg gctgccctgt ctcactgcag attcaggacc 3250

agcttgggct gcgtgcgttc tgccttgcca gtcagccgag gatgtagttg 3300

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actctaaggg atatcaacac tgcccagcac aggggccctg aatttatgtg 3700

gtttttatac attttttaat aagatgcact ttatgtcatt ttttaataaa 3750

gtctgaagaa ttactgttta aaaaaaaaa a 3781

<210> 253
<211> 837
<212> PRT
<213> Homo sapiens

<400> 253
Met Leu Arg Thr Ala Met Gly Leu Arg Ser Trp Leu Ala Ala Pro
1   5   10   15

Trp Gly Ala Leu Pro Pro Arg Pro Pro Leu Leu Leu Leu Leu Leu
                20   25   30

Leu Leu Leu Leu Leu Gln Pro Pro Pro Thr Trp Ala Leu Ser
                35   40   45

Pro Arg Ile Ser Leu Pro Leu Gly Ser Glu Glu Arg Pro Phe Leu
                50   55   60

Arg Phe Glu Ala Glu His Ile Ser Asn Tyr Thr Ala Leu Leu Leu
                65   70   75

Ser Arg Asp Gly Arg Thr Leu Tyr Val Gly Ala Arg Glu Ala Leu

238

Phe Ala Leu Ser Ser Asn Leu Ser Phe Leu Pro Gly Gly Glu Tyr
              95   100   105

Gln Glu Leu Leu Trp Gly Ala Asp Ala Glu Lys Lys Gln Gln Cys
              110   115   120

Ser Phe Lys Gly Lys Asp Pro Gln Arg Asp Cys Gln Asn Tyr Ile
              125   130   135

Lys Ile Leu Leu Pro Leu Ser Gly Ser His Leu Phe Thr Cys Gly
              140   145   150

Thr Ala Ala Phe Ser Pro Met Cys Thr Tyr Ile Asn Met Glu Asn
              155   160   165

Phe Thr Leu Ala Arg Asp Glu Lys Gly Asn Val Leu Leu Glu Asp
              170   175   180

Gly Lys Gly Arg Cys Pro Phe Asp Pro Asn Phe Lys Ser Thr Ala
              185   190   195

Leu Val Val Asp Gly Glu Leu Tyr Thr Gly Thr Val Ser Ser Phe
              200   205   210

Gln Gly Asn Asp Pro Ala Ile Ser Arg Ser Gln Ser Leu Arg Pro
              215   220   225

Thr Lys Thr Glu Ser Ser Leu Asn Trp Leu Gln Asp Pro Ala Phe
              230   235   240

Val Ala Ser Ala Tyr Ile Pro Glu Ser Leu Gly Ser Leu Gln Gly
              245   250   255

Asp Asp Asp Lys Ile Tyr Phe Phe Phe Ser Glu Thr Gly Gln Glu
              260   265   270

Phe Glu Phe Phe Glu Asn Thr Ile Val Ser Arg Ile Ala Arg Ile
              275   280   285

Cys Lys Gly Asp Glu Gly Gly Glu Arg Val Leu Gln Gln Arg Trp
              290   295   300

Thr Ser Phe Leu Lys Ala Gln Leu Leu Cys Ser Arg Pro Asp Asp
              305   310   315

Gly Phe Pro Phe Asn Val Leu Gln Asp Val Phe Thr Leu Ser Pro
              320   325   330

Ser Pro Gln Asp Trp Arg Asp Thr Leu Phe Tyr Gly Val Phe Thr
              335   340   345

Ser Gln Trp His Arg Gly Thr Thr Glu Gly Ser Ala Val Cys Val
              350   355   360

Phe Thr Met Lys Asp Val Gln Arg Val Phe Ser Gly Leu Tyr Lys
              365   370   375

239

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Glu Val Asn Arg Glu Thr Gln Gln Trp Tyr Thr Val Thr His Pro
            380             385             390

Val Pro Thr Pro Arg Pro Gly Ala Cys Ile Thr Asn Ser Ala Arg
            395             400             405

Glu Arg Lys Ile Asn Ser Ser Leu Gln Leu Pro Asp Arg Val Leu
            410             415             420

Asn Phe Leu Lys Asp His Phe Leu Met Asp Gly Gln Val Arg Ser
            425             430             435

Arg Met Leu Leu Leu Gln Pro Gln Ala Arg Tyr Gln Arg Val Ala
            440             445             450

Val His Arg Val Pro Gly Leu His His Thr Tyr Asp Val Leu Phe
            455             460             465

Leu Gly Thr Gly Asp Gly Arg Leu His Lys Ala Val Ser Val Gly
            470             475             480

Pro Arg Val His Ile Ile Glu Glu Leu Gln Ile Phe Ser Ser Gly
            485             490             495

Gln Pro Val Gln Asn Leu Leu Leu Asp Thr His Arg Gly Leu Leu
            500             505             510

Tyr Ala Ala Ser His Ser Gly Val Val Gln Val Pro Met Ala Asn
            515             520             525

Cys Ser Leu Tyr Arg Ser Cys Gly Asp Cys Leu Leu Ala Arg Asp
            530             535             540

Pro Tyr Cys Ala Trp Ser Gly Ser Ser Cys Lys His Val Ser Leu
            545             550             555

Tyr Gln Pro Gln Leu Ala Thr Arg Pro Trp Ile Gln Asp Ile Glu
            560             565             570

Gly Ala Ser Ala Lys Asp Leu Cys Ser Ala Ser Ser Val Val Ser
            575             580             585

Pro Ser Phe Val Pro Thr Gly Glu Lys Pro Cys Glu Gln Val Gln
            590             595             600

Phe Gln Pro Asn Thr Val Asn Thr Leu Ala Cys Pro Leu Leu Ser
            605             610             615

Asn Leu Ala Thr Arg Leu Trp Leu Arg Asn Gly Ala Pro Val Asn
            620             625             630

Ala Ser Ala Ser Cys His Val Leu Pro Thr Gly Asp Leu Leu Leu
            635             640             645

Val Gly Thr Gln Gln Leu Gly Glu Phe Gln Cys Trp Ser Leu Glu
            650             655             660

Glu Gly Phe Gln Gln Leu Val Ala Ser Tyr Cys Pro Glu Val Val
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240

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                665                    670                    675
Glu Asp Gly Val Ala Asp Gln Thr Asp Glu Gly Gly Ser Val Pro
                680                    685                    690

Val Ile Ile Ser Thr Ser Arg Val Ser Ala Pro Ala Gly Gly Lys
                695                    700                    705

Ala Ser Trp Gly Ala Asp Arg Ser Tyr Trp Lys Glu Phe Leu Val
                710                    715                    720

Met Cys Thr Leu Phe Val Leu Ala Val Leu Leu Pro Val Leu Phe
                725                    730                    735

Leu Leu Tyr Arg His Arg Asn Ser Met Lys Val Phe Leu Lys Gln
                740                    745                    750

Gly Glu Cys Ala Ser Val His Pro Lys Thr Cys Pro Val Val Leu
                755                    760                    765

Pro Pro Glu Thr Arg Pro Leu Asn Gly Leu Gly Pro Pro Ser Thr
                770                    775                    780

Pro Leu Asp His Arg Gly Tyr Gln Ser Leu Ser Asp Ser Pro Pro
                785                    790                    795

Gly Ala Arg Val Phe Thr Glu Ser Glu Lys Arg Pro Leu Ser Ile
                800                    805                    810

Gln Asp Ser Phe Val Glu Val Ser Pro Val Cys Pro Arg Pro Arg
                815                    820                    825

Val Arg Leu Gly Ser Glu Ile Arg Asp Ser Val Val
                830                    835

<210> 254
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 254
 agcccgtgca gaatctgctc ctgg 24

<210> 255
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.
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241

<400> 255
tgaagccagg gcagcgtcct ctgg 24

<210> 256
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 256
gtacaggctg cagttggc 18

<210> 257
<211> 41
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-41
<223> Synthetic construct.

<400> 257
agaagccatg tgagcaagtc cagttccagc ccaacacagt g 41

<210> 258
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 258
gagctgcaga tcttctcatc gggacagccc gtgcagaatc tgctc 45

<210> 259
<211> 4563
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 3635
<223> unknown base

<400> 259
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cggggacagg cgccgtgcga accgagccca gccagccgga ggacgcgggc 100

agggcgggac gggagcccgg actcgtctgc cgccgccgtc gtcgccgtcg 150

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tgccggcccc gcgtccccgc gcgcgagcgg gaggagccgc cgccacctcg 200

cgcccgagcc gccgctagcg cgcgccgggc atggtcccct cttaaaggcg 250

caggccgcgg cggcgggggc gggtgtgcgg aacaaagcgc cggcgcgggg 300

cctgcgggcg gctcggggggc cgcgatgggc gcggcgggcc cgcggcggcg 350

gcggcgctgc ccgggccggg cctcgcggcg ctagggcggg ctggcctccg 400

tgggcggggg cagcgggctg agggcgcgcg gagcctgcgg cggcggcggc 450

ggcggcggcg gcggcccggc gggcggagcg gcgcgggcat ggccgcgcgc 500

ggccggcgcg cctggctcag cgtgctgctc gggctcgtcc tgggcttcgt 550

gctggcctcg cggctcgtcc tgccccgggc ttccgagctg aagcgagcgg 600

gcccacggcg ccgcgccagc cccgagggct gccggtccgg gcaggcggcg 650

gcttcccagg ccggcggggc gcgcggcgat gcgcgcgggg cgcagctctg 700

gccgcccggc tcggacccag atggcggccc gcgcgacagg aactttctct 750

tcgtgggagt catgaccgcc cagaaatacc tgcagactcg ggccgtggcc 800

gcctacagaa catggtccaa gacaattcct gggaaagttc agttcttctc 850

aagtgagggt tctgacacat ctgtaccaat tccagtagtg ccactacggg 900

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acattagaga tctccataac agtaaaattc accaagctat cacattacac 1400

cccaacaaaa acccacccta ccagtacagg ctccacagct acatgctgag 1450

ccgcaagata tccgagctcc gccatcgcac aatacagctg caccgcgaaa 1500

ttgtcctgat gagcaaatac agcaacacag aaattcataa agaggacctc 1550

cagctgggaa tccctccctc cttcatgagg tttcagcccc gccagcgaga 1600
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243

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ggagattctg gaatgggagt ttctgactgg aaaatacttg tattcggcag 1650

ttgacggcca gccccctcga agaggaatgg actccgccca gagggaagcc 1700

ttggacgaca ttgtcatgca ggtcatggag atgatcaatg ccaacgccaa 1750

gaccagaggg cgcatcattg acttcaaaga gatccagtac ggctaccgcc 1800

gggtgaaccc catgtatggg gctgagtaca tcctggacct gctgcttctg 1850

tacaaaaagc acaaagggaa gaaaatgacg gtccctgtga ggaggcacgc 1900

gtatttacag cagactttca gcaaaatcca gtttgtggag catgaggagc 1950

tggatgcaca agagttggcc aagagaatca atcaggaatc tggatccttg 2000

tcctttctct caaactccct gaagaagctc gtcccctttc agctccctgg 2050

gtcgaagagt gagcacaaag aacccaaaga taaaaagata aacatactga 2100

ttcctttgtc tgggcgtttc gacatgtttg tgagatttat gggaaacttt 2150

gagaagacgt gtcttatccc caatcagaac gtcaagctcg tggttctgct 2200

tttcaattct gactccaacc ctgacaaggc caaacaagtt gaactgatga 2250

gagattaccg cattaagtac cctaaagccg acatgcagat tttgcctgtg 2300

tctggagagt tttcaagagc cctggccctg gaagtaggat cctcccagtt 2350

taacaatgaa tctttgctct tcttctgcga cgtcgacctc gtgtttacta 2400

cagaattcct tcagcgatgt cgagcaaata cagttctggg ccaacaaata 2450

tattttccaa tcatcttcag ccagtatgac ccaaagattg tttatagtgg 2500

gaaagttccc agtgacaacc attttgcctt tactcagaaa actggcttct 2550

ggagaaacta tgggtttggc atcacgtgta tttataaggg agatcttgtc 2600

cgagtgggtg gctttgatgt ttccatccaa ggctgggggc tggaggatgt 2650

ggaccttttc aacaaggttg tccaggcagg tttgaagacg tttaggagcc 2700

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cttgacccca aacagtacaa aatgtgcttg gggtccaaag catcgaccta 2800

tgggtccacc cagcagctgg ctgagatgtg gctggaaaaa aatgatccaa 2850

gttacagtaa aagcagcaat aataatggct cagtgaggac agcctaatgt 2900

ccagctttgc tggaaaagac gttttttaatt atctaattta ttttttcaaaa 2950

atttttttgta tgatcagttt ttgaagtccg tatacaagga tatattttac 3000

aagtggtttt cttacatagg actcctttaa gattgagctt tctgaacaag 3050
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244

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aaggtgatca gtgtttgcct ttgaacacat cttcttgctg aacattatgt 3100

agcagacctg cttaactttg acttgaaatg tacctgatga acaaaacttt 3150

tttaaaaaaa tgttttcttt tgagaccctt tgctccagtc ctatggcaga 3200

aaacgtgaac attcctgcaa agtattattg taacaaaaca ctgtaactct 3250

ggtaaatgtt ctgttgtgat tgttaacatt ccacagattc tacctttgt 3300

gttttgtttt ttttttttac aattgtttta aagccatttc atgttccagt 3350

tgtaagataa ggaaatgtga taatagctgt ttcatcattg tcttcaggag 3400

agctttccag agttgatcat ttcctctcat ggtactctgc tcagcatggc 3450

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tcactctgtt acccaggctg gaatgcagtg gcgcaatctt ggctcacttt 3550

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agctgggatt acaggcacac accaccacgc ccagntagtt tttttgtatt 3650

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tggagggctg cgtatttgta aatagcctga tgctcatttg gaaaaataaa 4450

ccagtgaaca atattttct attgtacttt tcgaaccatt ttgtctcatt 4500
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245

attcctgttt tagctgaaga attgtattac atttggagag taaaaaactt 4550

aaacacgaaa aaa 4563

<210> 260
<211> 802
<212> PRT
<213> Homo sapiens

<400> 260

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Met Ala Ala Arg Gly Arg Arg Ala Trp Leu Ser Val Leu Leu Gly
1               5                   10                  15

Leu Val Leu Gly Phe Val Leu Ala Ser Arg Leu Val Leu Pro Arg
            20                  25                  30

Ala Ser Glu Leu Lys Arg Ala Gly Pro Arg Arg Arg Ala Ser Pro
            35                  40                  45

Glu Gly Cys Arg Ser Gly Gln Ala Ala Ala Ser Gln Ala Gly Gly
            50                  55                  60

Ala Arg Gly Asp Ala Arg Gly Ala Gln Leu Trp Pro Pro Gly Ser
            65                  70                  75

Asp Pro Asp Gly Gly Pro Arg Asp Arg Asn Phe Leu Phe Val Gly
            80                  85                  90

Val Met Thr Ala Gln Lys Tyr Leu Gln Thr Arg Ala Val Ala Ala
            95                  100                 105

Tyr Arg Thr Trp Ser Lys Thr Ile Pro Gly Lys Val Gln Phe Phe
            110                 115                 120

Ser Ser Glu Gly Ser Asp Thr Ser Val Pro Ile Pro Val Val Pro
            125                 130                 135

Leu Arg Gly Val Asp Asp Ser Tyr Pro Pro Gln Lys Lys Ser Phe
            140                 145                 150

Met Met Leu Lys Tyr Met His Asp His Tyr Leu Asp Lys Tyr Glu
            155                 160                 165

Trp Phe Met Arg Ala Asp Asp Asp Val Tyr Ile Lys Gly Asp Arg
            170                 175                 180

Leu Glu Asn Phe Leu Arg Ser Leu Asn Ser Ser Glu Pro Leu Phe
            185                 190                 195

Leu Gly Gln Thr Gly Leu Gly Thr Thr Glu Glu Met Gly Lys Leu
            200                 205                 210

Ala Leu Glu Pro Gly Glu Asn Phe Cys Met Gly Gly Pro Gly Val
            215                 220                 225

Ile Met Ser Arg Glu Val Leu Arg Arg Met Val Pro His Ile Gly
            230                 235                 240
```

246

Lys Cys Leu Arg Glu Met Tyr Thr Thr His Glu Asp Val Glu Val
                245   250   255

Gly Arg Cys Val Arg Arg Phe Ala Gly Val Gln Cys Val Trp Ser
                260   265   270

Tyr Glu Met Arg Gln Leu Phe Tyr Glu Asn Tyr Glu Gln Asn Lys
                275   280   285

Lys Gly Tyr Ile Arg Asp Leu His Asn Ser Lys Ile His Gln Ala
                290   295   300

Ile Thr Leu His Pro Asn Lys Asn Pro Pro Tyr Gln Tyr Arg Leu
                305   310   315

His Ser Tyr Met Leu Ser Arg Lys Ile Ser Glu Leu Arg His Arg
                320   325   330

Thr Ile Gln Leu His Arg Glu Ile Val Leu Met Ser Lys Tyr Ser
                335   340   345

Asn Thr Glu Ile His Lys Glu Asp Leu Gln Leu Gly Ile Pro Pro
                350   355   360

Ser Phe Met Arg Phe Gln Pro Arg Gln Arg Glu Glu Ile Leu Glu
                365   370   375

Trp Glu Phe Leu Thr Gly Lys Tyr Leu Tyr Ser Ala Val Asp Gly
                380   385   390

Gln Pro Pro Arg Arg Gly Met Asp Ser Ala Gln Arg Glu Ala Leu
                395   400   405

Asp Asp Ile Val Met Gln Val Met Glu Met Ile Asn Ala Asn Ala
                410   415   420

Lys Thr Arg Gly Arg Ile Ile Asp Phe Lys Glu Ile Gln Tyr Gly
                425   430   435

Tyr Arg Arg Val Asn Pro Met Tyr Gly Ala Glu Tyr Ile Leu Asp
                440   445   450

Leu Leu Leu Leu Tyr Lys Lys His Lys Gly Lys Lys Met Thr Val
                455   460   465

Pro Val Arg Arg His Ala Tyr Leu Gln Gln Thr Phe Ser Lys Ile
                470   475   480

Gln Phe Val Glu His Glu Glu Leu Asp Ala Gln Glu Leu Ala Lys
                485   490   495

Arg Ile Asn Gln Glu Ser Gly Ser Leu Ser Phe Leu Ser Asn Ser
                500   505   510

Leu Lys Lys Leu Val Pro Phe Gln Leu Pro Gly Ser Lys Ser Glu
                515   520   525

His Lys Glu Pro Lys Asp Lys Lys Ile Asn Ile Leu Ile Pro Leu

Ser Gly Arg Phe Asp Met Phe Val Arg Phe Met Gly Asn Phe Glu
                    545   550   555

Lys Thr Cys Leu Ile Pro Asn Gln Asn Val Lys Leu Val Val Leu
                    560   565   570

Leu Phe Asn Ser Asp Ser Asn Pro Asp Lys Ala Lys Gln Val Glu
                    575   580   585

Leu Met Arg Asp Tyr Arg Ile Lys Tyr Pro Lys Ala Asp Met Gln
                    590   595   600

Ile Leu Pro Val Ser Gly Glu Phe Ser Arg Ala Leu Ala Leu Glu
                    605   610   615

Val Gly Ser Ser Gln Phe Asn Asn Glu Ser Leu Leu Phe Phe Cys
                    620   625   630

Asp Val Asp Leu Val Phe Thr Thr Glu Phe Leu Gln Arg Cys Arg
                    635   640   645

Ala Asn Thr Val Leu Gly Gln Gln Ile Tyr Phe Pro Ile Ile Phe
                    650   655   660

Ser Gln Tyr Asp Pro Lys Ile Val Tyr Ser Gly Lys Val Pro Ser
                    665   670   675

Asp Asn His Phe Ala Phe Thr Gln Lys Thr Gly Phe Trp Arg Asn
                    680   685   690

Tyr Gly Phe Gly Ile Thr Cys Ile Tyr Lys Gly Asp Leu Val Arg
                    695   700   705

Val Gly Gly Phe Asp Val Ser Ile Gln Gly Trp Gly Leu Glu Asp
                    710   715   720

Val Asp Leu Phe Asn Lys Val Val Gln Ala Gly Leu Lys Thr Phe
                    725   730   735

Arg Ser Gln Glu Val Gly Val Val His Val His His Pro Val Phe
                    740   745   750

Cys Asp Pro Asn Leu Asp Pro Lys Gln Tyr Lys Met Cys Leu Gly
                    755   760   765

Ser Lys Ala Ser Thr Tyr Gly Ser Thr Gln Gln Leu Ala Glu Met
                    770   775   780

Trp Leu Glu Lys Asn Asp Pro Ser Tyr Ser Lys Ser Ser Asn Asn
                    785   790   795

Asn Gly Ser Val Arg Thr Ala
                    800

<210> 261
<211> 24

<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 261
 gtgccactac ggggtgtgga cgac 24

<210> 262
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 262
 tcccatttct tccgtggtgc ccag 24

<210> 263
<211> 46
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-46
<223> Synthetic construct.

<400> 263
 ccagaagaag tccttcatga tgctcaagta catgcacgac cactac 46

<210> 264
<211> 1419
<212> DNA
<213> Homo sapiens

<400> 264
 ggacaaccgt tgctgggtgt cccagggcct gaggcaggac ggtactccgc 50

 tgacaccttc cctttcggcc ttgaggttcc cagcctggtg gccccaggac 100

 gttccggtcg catggcagag tgctacggac gacgcctatg aagcccttag 150

 tccttctagt tgcgcttttg ctatggcctt cgtctgtgcc ggcttatccg 200

 agcataactg tgacacctga tgaagagcaa aacttgaatc attatataca 250

 agttttagag aacctagtac gaagtgttcc ctctggggag ccaggtcgtg 300

 agaaaaaatc taactctcca aaacatgttt attctatagc atcaaaggga 350

 tcaaaattta aggagctagt tacacatgga gacgcttcaa ctgagaatga 400

249

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tgttttaacc aatcctatca gtgaagaaac tacaactttc cctacaggag 450

gcttcacacc ggaaatagga aagaaaaaac acacggaaag taccccattc 500

tggtcgatca aaccaaacaa tgtttccatt gttttgcatg cagaggaacc 550

ttatattgaa aatgaagagc cagagccaga gccggagcca gctgcaaaac 600

aaactgaggc accaagaatg ttgccagttg ttactgaatc atctacaagt 650

ccatatgtta cctcatacaa gtcacctgtc accactttag ataagagcac 700

tggcattgag atctctacag aatcagaaga tgttcctcag ctctcaggtg 750

aaactgcgat agaaaaaccc gaagagtttg gaaagcaccc agagagttgg 800

aataatgatg acattttgaa aaaaatttta gatattaatt cacaagtgca 850

acaggcactt cttagtgaca ccagcaaccc agcatataga gaagatattg 900

aagcctctaa agatcaccta aaacgaagcc ttgctctagc agcagcagca 950

gaacataaat taaaaacaat gtataagtcc cagttattgc cagtaggacg 1000

aacaagtaat aaaattgatg acatcgaaac tgttattaac atgctgtgta 1050

attctagatc taaactctat gaatatttag atattaaatg tgttccacca 1100

gagatgagag aaaaagctgc tacagtattc aatacattaa aaaatatgtg 1150

tagatcaagg agagtcacag ccttattaaa agtttattaa acaataatat 1200

aaaaatttta aacctacttg atattccata acaaagctga tttaagcaaa 1250

ctgcattttt tcacaggaga aataatcata ttcgtaattt caaaagttgt 1300

ataaaaatat tttctattgt agttcaaatg tgccaacatc tttatgtgtc 1350

atgtgttatg aacaattttc atatgcacta aaaacctaat ttaaaataaa 1400

attttggttc aggaaaaaa 1419
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<210> 265
<211> 350
<212> PRT
<213> Homo sapiens

<400> 265

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Met Lys Pro Leu Val Leu Leu Val Ala Leu Leu Leu Trp Pro Ser
  1               5                  10                  15

Ser Val Pro Ala Tyr Pro Ser Ile Thr Val Thr Pro Asp Glu Glu
               20                  25                  30

Gln Asn Leu Asn His Tyr Ile Gln Val Leu Glu Asn Leu Val Arg
               35                  40                  45

Ser Val Pro Ser Gly Glu Pro Gly Arg Glu Lys Lys Ser Asn Ser
```

250

Pro Lys His Val Tyr Ser Ile Ala Ser Lys Gly Ser Lys Phe Lys
                    65   70   75

Glu Leu Val Thr His Gly Asp Ala Ser Thr Glu Asn Asp Val Leu
                    80   85   90

Thr Asn Pro Ile Ser Glu Glu Thr Thr Thr Phe Pro Thr Gly Gly
                    95   100   105

Phe Thr Pro Glu Ile Gly Lys Lys Lys His Thr Glu Ser Thr Pro
                   110   115   120

Phe Trp Ser Ile Lys Pro Asn Asn Val Ser Ile Val Leu His Ala
                   125   130   135

Glu Glu Pro Tyr Ile Glu Asn Glu Glu Pro Glu Pro Glu Pro Glu
                   140   145   150

Pro Ala Ala Lys Gln Thr Glu Ala Pro Arg Met Leu Pro Val Val
                   155   160   165

Thr Glu Ser Ser Thr Ser Pro Tyr Val Thr Ser Tyr Lys Ser Pro
                   170   175   180

Val Thr Thr Leu Asp Lys Ser Thr Gly Ile Glu Ile Ser Thr Glu
                   185   190   195

Ser Glu Asp Val Pro Gln Leu Ser Gly Glu Thr Ala Ile Glu Lys
                   200   205   210

Pro Glu Glu Phe Gly Lys His Pro Glu Ser Trp Asn Asn Asp Asp
                   215   220   225

Ile Leu Lys Lys Ile Leu Asp Ile Asn Ser Gln Val Gln Gln Ala
                   230   235   240

Leu Leu Ser Asp Thr Ser Asn Pro Ala Tyr Arg Glu Asp Ile Glu
                   245   250   255

Ala Ser Lys Asp His Leu Lys Arg Ser Leu Ala Leu Ala Ala Ala
                   260   265   270

Ala Glu His Lys Leu Lys Thr Met Tyr Lys Ser Gln Leu Leu Pro
                   275   280   285

Val Gly Arg Thr Ser Asn Lys Ile Asp Asp Ile Glu Thr Val Ile
                   290   295   300

Asn Met Leu Cys Asn Ser Arg Ser Lys Leu Tyr Glu Tyr Leu Asp
                   305   310   315

Ile Lys Cys Val Pro Pro Glu Met Arg Glu Lys Ala Ala Thr Val
                   320   325   330

Phe Asn Thr Leu Lys Asn Met Cys Arg Ser Arg Arg Val Thr Ala
                   335   340   345

251

Leu Leu Lys Val Tyr
                350

<210> 266
<211> 2403
<212> DNA
<213> Homo sapiens

<400> 266
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acagctggcc tgacctccaa atcatccatc cacccctgct gtcatctgtt 100

ttcatagtgt gagatcaacc cacaggaata tccatggctt ttgtgctcat 150

tttggttctc agtttctacg agctggtgtc aggacagtgg caagtcactg 200

gaccgggcaa gtttgtccag gccttggtgg gggaggacgc cgtgttctcc 250

tgctccctct ttcctgagac cagtgcagag gctatggaag tgcggttctt 300

caggaatcag ttccatgctg tggtccacct ctacagagat ggggaagact 350

gggaatctaa gcagatgcca cagtatcgag ggagaactga gtttgtgaag 400

gactccattg caggggggcg tgtctctcta aggctaaaaa acatcactcc 450

ctcggacatc ggcctgtatg ggtgctggtt cagttcccag atttacgatg 500

aggaggccac ctgggagctg cgggtggcag cactgggctc acttcctctc 550

atttccatcg tgggatatgt tgacggaggt atccagttac tctgcctgtc 600

ctcaggctgg ttcccccagc ccacagccaa gtggaaaggt ccacaaggac 650

aggatttgtc ttcagactcc agagcaaatg cagatgggta cagcctgtat 700

gatgtggaga tctccattat agtccaggaa aatgctggga gcatattgtg 750

ttccatccac cttgctgagc agagtcatga ggtggaatcc aaggtattga 800

taggagagac gtttttccag ccctcacctt ggcgcctggc ttctatttta 850

ctcgggttac tctgtggtgc cctgtgtggt gttgtcatgg ggatgataat 900

tgttttcttc aaatccaaag ggaaaatcca ggcggaactg gactggagaa 950

gaaagcacgg acaggcagaa ttgagagacg cccggaaaca cgcagtggag 1000

gtgactctgg atccagagac ggctcacccg aagctctgcg tttctgatct 1050

gaaaactgta acccatagaa aagctcccca ggaggtgcct cactctgaga 1100

agagatttac aaggaagagt gtggtggctt ctcagggttt ccaagcaggg 1150

agacattact gggaggtgga cgtgggacaa aatgtagggt ggtatgtggg 1200

agtgtgtcgg gatgacgtag acagggggaa gaacaatgtg actttgtctc 1250

252

```
ccaacaatgg gtattgggtc ctcagactga caacagaaca tttgtatttc 1300

acattcaatc cccattttat cagcctcccc cccagcaccc ctcctacacg 1350

agtaggggtc ttcctggact atgagggtgg gaccatctcc ttcttcaata 1400

caaatgacca gtcccttatt tataccctgc tgacatgtca gtttgaaggc 1450

ttgttgagac cctatatcca gcatgcgatg tatgacgagg aaaaggggac 1500

tcccatattc atatgtccag tgtcctgggg atgagacaga gaagaccctg 1550

cttaaagggc cccacaccac agacccagac acagccaagg gagagtgctc 1600

ccgacaggtg gccccagctt cctctccgga gcctgcgcac agagagtcac 1650

gcccccccact ctcctttagg gagctgaggt tcttctgccc tgagccctgc 1700

agcagcggca gtcacagctt ccagatgagg ggggattggc ctgaccctgt 1750

gggagtcaga agccatggct gccctgaagt ggggacggaa tagactcaca 1800

ttaggtttag tttgtgaaaa ctccatccag ctaagcgatc ttgaacaagt 1850

cacaacctcc caggctcctc atttgctagt cacggacagt gattcctgcc 1900

tcacaggtga agattaaaga gacaacgaat gtgaatcatg cttgcaggtt 1950

tgagggcaca gtgtttgcta atgatgtgtt tttatattat acattttccc 2000

accataaact ctgtttgctt attccacatt aatttacttt tctctatacc 2050

aaatcaccca tggaatagtt attgaacacc tgctttgtga ggctcaaaga 2100

ataaagagga ggtaggattt ttcactgatt ctataagccc agcattacct 2150

gataccaaaa ccaggcaaag aaaacagaag aagaggaagg aaaactacag 2200

gtccatatcc ctcattaaca cagacacaaa aattctaaat aaaattttaa 2250

caaattaaac taaacaatat atttaaagat gatatataac tactcagtgt 2300

ggtttgtccc acaaatgcag agttggttta atatttaaat atcaaccagt 2350

gtaattcagc acattaataa agtaaaaaag aaaaccataa aaaaaaaaaa 2400

aaa 2403
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<210> 267
<211> 466
<212> PRT
<213> Homo sapiens

<400> 267
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 Met Ala Phe Val Leu Ile Leu Val Leu Ser Phe Tyr Glu Leu Val
  1               5                  10                  15

 Ser Gly Gln Trp Gln Val Thr Gly Pro Gly Lys Phe Val Gln Ala
```

```
                   20                    25                    30
Leu Val Gly Glu Asp Ala Val Phe Ser Cys Ser Leu Phe Pro Glu
                   35                    40                    45

Thr Ser Ala Glu Ala Met Glu Val Arg Phe Phe Arg Asn Gln Phe
                   50                    55                    60

His Ala Val Val His Leu Tyr Arg Asp Gly Glu Asp Trp Glu Ser
                   65                    70                    75

Lys Gln Met Pro Gln Tyr Arg Gly Arg Thr Glu Phe Val Lys Asp
                   80                    85                    90

Ser Ile Ala Gly Gly Arg Val Ser Leu Arg Leu Lys Asn Ile Thr
                   95                    100                   105

Pro Ser Asp Ile Gly Leu Tyr Gly Cys Trp Phe Ser Ser Gln Ile
                   110                   115                   120

Tyr Asp Glu Glu Ala Thr Trp Glu Leu Arg Val Ala Ala Leu Gly
                   125                   130                   135

Ser Leu Pro Leu Ile Ser Ile Val Gly Tyr Val Asp Gly Gly Ile
                   140                   145                   150

Gln Leu Leu Cys Leu Ser Ser Gly Trp Phe Pro Gln Pro Thr Ala
                   155                   160                   165

Lys Trp Lys Gly Pro Gln Gly Gln Asp Leu Ser Ser Asp Ser Arg
                   170                   175                   180

Ala Asn Ala Asp Gly Tyr Ser Leu Tyr Asp Val Glu Ile Ser Ile
                   185                   190                   195

Ile Val Gln Glu Asn Ala Gly Ser Ile Leu Cys Ser Ile His Leu
                   200                   205                   210

Ala Glu Gln Ser His Glu Val Glu Ser Lys Val Leu Ile Gly Glu
                   215                   220                   225

Thr Phe Phe Gln Pro Ser Pro Trp Arg Leu Ala Ser Ile Leu Leu
                   230                   235                   240

Gly Leu Leu Cys Gly Ala Leu Cys Gly Val Val Met Gly Met Ile
                   245                   250                   255

Ile Val Phe Phe Lys Ser Lys Gly Lys Ile Gln Ala Glu Leu Asp
                   260                   265                   270

Trp Arg Arg Lys His Gly Gln Ala Glu Leu Arg Asp Ala Arg Lys
                   275                   280                   285

His Ala Val Glu Val Thr Leu Asp Pro Glu Thr Ala His Pro Lys
                   290                   295                   300

Leu Cys Val Ser Asp Leu Lys Thr Val Thr His Arg Lys Ala Pro
                   305                   310                   315

                               254
```

```
Gln Glu Val Pro His Ser Glu Lys Arg Phe Thr Arg Lys Ser Val
            320                 325                 330

Val Ala Ser Gln Gly Phe Gln Ala Gly Arg His Tyr Trp Glu Val
            335                 340                 345

Asp Val Gly Gln Asn Val Gly Trp Tyr Val Gly Val Cys Arg Asp
            350                 355                 360

Asp Val Asp Arg Gly Lys Asn Asn Val Thr Leu Ser Pro Asn Asn
            365                 370                 375

Gly Tyr Trp Val Leu Arg Leu Thr Thr Glu His Leu Tyr Phe Thr
            380                 385                 390

Phe Asn Pro His Phe Ile Ser Leu Pro Pro Ser Thr Pro Pro Thr
            395                 400                 405

Arg Val Gly Val Phe Leu Asp Tyr Glu Gly Gly Thr Ile Ser Phe
            410                 415                 420

Phe Asn Thr Asn Asp Gln Ser Leu Ile Tyr Thr Leu Leu Thr Cys
            425                 430                 435

Gln Phe Glu Gly Leu Leu Arg Pro Tyr Ile Gln His Ala Met Tyr
            440                 445                 450

Asp Glu Glu Lys Gly Thr Pro Ile Phe Ile Cys Pro Val Ser Trp
            455                 460                 465

Gly
```

<210> 268
<211> 2103
<212> DNA
<213> Homo sapiens

<400> 268
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tggtgagggc taggaaaaga gtttgttggg aaccctgggt tatcggcctc 100

gtcatcttca tatccctgat tgtcctggca gtgtgcattg gactcactgt 150

tcattatgtg agatataatc aaaagaagac ctacaattac tatagcacat 200

tgtcatttac aactgacaaa ctatatgctg agtttggcag agaggcttct 250

aacaatttta cagaaatgag ccagagactt gaatcaatgg tgaaaaatgc 300

attttataaa tctccattaa gggaagaatt tgtcaagtct caggttatca 350

agttcagtca acagaagcat ggagtgttgg ctcatatgct gttgatttgt 400

agatttcact ctactgagga tcctgaaact gtagataaaa ttgttcaact 450

tgttttacat gaaaagctgc aagatgctgt aggaccccct aaagtagatc 500
```

255

```
ctcactcagt taaaattaaa aaaatcaaca agacagaaac agacagctat 550

ctaaaccatt gctgcggaac acgaagaagt aaaactctag gtcagagtct 600

caggatcgtt ggtgggacag aagtagaaga gggtgaatgg ccctggcagg 650

ctagcctgca gtgggatggg agtcatcgct gtggagcaac cttaattaat 700

gccacatggc ttgtgagtgc tgctcactgt tttacaacat ataagaaccc 750

tgccagatgg actgcttcct ttggagtaac aataaaacct tcgaaaatga 800

aacggggtct ccggagaata attgtccatg aaaaatacaa acacccatca 850

catgactatg atatttctct tgcagagctt tctagccctg ttccctacac 900

aaatgcagta catagagttt gtctccctga tgcatcctat gagtttcaac 950

caggtgatgt gatgtttgtg acaggatttg gagcactgaa aaatgatggt 1000

tacagtcaaa atcatcttcg acaagcacag gtgactctca tagacgctac 1050

aacttgcaat gaacctcaag cttacaatga cgccataact cctagaatgt 1100

tatgtgctgg ctccttagaa ggaaaaacag atgcatgcca gggtgactct 1150

ggaggaccac tggttagttc agatgctaga gatatctggt accttgctgg 1200

aatagtgagc tggggagatg aatgtgcgaa acccaacaag cctggtgttt 1250

atactagagt tacggccttg cgggactgga ttacttcaaa aactggtatc 1300

taagagacaa aagcctcatg aacagataa cattttttt tgttttttgg 1350

gtgtggaggc cattttaga gatacagaat tggagaagac ttgcaaaaca 1400

gctagatttg actgatctca ataaactgtt tgcttgatgc atgtattttc 1450

ttcccagctc tgttccgcac gtaagcatcc tgcttctgcc agatcaactc 1500

tgtcatctgt gagcaatagt tgaaacttta tgtacataga gaaatagata 1550

atacaatatt acattacagc ctgtattcat ttgttctcta gaagttttgt 1600

cagaattttg acttgttgac ataaatttgt aatgcatata tacaatttga 1650

agcactcctt ttcttcagtt cctcagctcc tctcatttca gcaaatatcc 1700

attttcaagg tgcagaacaa ggagtgaaag aaaatataag aagaaaaaaa -1750

tcccctacat tttattggca cagaaaagta ttaggtgttt ttcttagtgg 1800

aatattagaa atgatcatat tcattatgaa aggtcaagca aagacagcag 1850

aataccaatc acttcatcat ttaggaagta tgggaactaa gttaaggaag 1900

tccagaaaga agccaagata tatccttatt ttcatttcca aacaactact 1950
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256

atgataaatg tgaagaagat tctgttttt tgtgacctat aataattata 2000

caaacttcat gcaatgtact tgttctaagc aaattaaagc aaatatttat 2050

ttaacattgt tactgaggat gtcaacatat aacaataaaa tataaatcac 2100

cca 2103

<210> 269
<211> 423
<212> PRT
<213> Homo sapiens

<400> 269

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Met Met Tyr Arg Pro Asp Val Val Arg Ala Arg Lys Arg Val Cys
 1               5                  10                  15

Trp Glu Pro Trp Val Ile Gly Leu Val Ile Phe Ile Ser Leu Ile
                20                  25                  30

Val Leu Ala Val Cys Ile Gly Leu Thr Val His Tyr Val Arg Tyr
                35                  40                  45

Asn Gln Lys Lys Thr Tyr Asn Tyr Tyr Ser Thr Leu Ser Phe Thr
                50                  55                  60

Thr Asp Lys Leu Tyr Ala Glu Phe Gly Arg Glu Ala Ser Asn Asn
                65                  70                  75

Phe Thr Glu Met Ser Gln Arg Leu Glu Ser Met Val Lys Asn Ala
                80                  85                  90

Phe Tyr Lys Ser Pro Leu Arg Glu Glu Phe Val Lys Ser Gln Val
                95                 100                 105

Ile Lys Phe Ser Gln Gln Lys His Gly Val Leu Ala His Met Leu
               110                 115                 120

Leu Ile Cys Arg Phe His Ser Thr Glu Asp Pro Glu Thr Val Asp
               125                 130                 135

Lys Ile Val Gln Leu Val Leu His Glu Lys Leu Gln Asp Ala Val
               140                 145                 150

Gly Pro Pro Lys Val Asp Pro His Ser Val Lys Ile Lys Lys Ile
               155                 160                 165

Asn Lys Thr Glu Thr Asp Ser Tyr Leu Asn His Cys Cys Gly Thr
               170                 175                 180

Arg Arg Ser Lys Thr Leu Gly Gln Ser Leu Arg Ile Val Gly Gly
               185                 190                 195

Thr Glu Val Glu Glu Gly Glu Trp Pro Trp Gln Ala Ser Leu Gln
               200                 205                 210

Trp Asp Gly Ser His Arg Cys Gly Ala Thr Leu Ile Asn Ala Thr
               215                 220                 225
```

257

```
Trp Leu Val Ser Ala Ala His Cys Phe Thr Thr Tyr Lys Asn Pro
                230                 235                 240

Ala Arg Trp Thr Ala Ser Phe Gly Val Thr Ile Lys Pro Ser Lys
                245                 250                 255

Met Lys Arg Gly Leu Arg Arg Ile Ile Val His Glu Lys Tyr Lys
                260                 265                 270

His Pro Ser His Asp Tyr Asp Ile Ser Leu Ala Glu Leu Ser Ser
                275                 280                 285

Pro Val Pro Tyr Thr Asn Ala Val His Arg Val Cys Leu Pro Asp
                290                 295                 300

Ala Ser Tyr Glu Phe Gln Pro Gly Asp Val Met Phe Val Thr Gly
                305                 310                 315

Phe Gly Ala Leu Lys Asn Asp Gly Tyr Ser Gln Asn His Leu Arg
                320                 325                 330

Gln Ala Gln Val Thr Leu Ile Asp Ala Thr Thr Cys Asn Glu Pro
                335                 340                 345

Gln Ala Tyr Asn Asp Ala Ile Thr Pro Arg Met Leu Cys Ala Gly
                350                 355                 360

Ser Leu Glu Gly Lys Thr Asp Ala Cys Gln Gly Asp Ser Gly Gly
                365                 370                 375

Pro Leu Val Ser Ser Asp Ala Arg Asp Ile Trp Tyr Leu Ala Gly
                380                 385                 390

Ile Val Ser Trp Gly Asp Glu Cys Ala Lys Pro Asn Lys Pro Gly
                395                 400                 405

Val Tyr Thr Arg Val Thr Ala Leu Arg Asp Trp Ile Thr Ser Lys
                410                 415                 420

Thr Gly Ile
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<210> 270
<211> 1170
<212> DNA
<213> Homo sapiens

<400> 270
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aacctgacag cacagcctga gatcttgggg atccctcagc ctaacaccca 100

cagacgtcag ctggtggatt cccgctgcat caaggcctac ccactgtctc 150

catgctgggc tctccctgcc ttctgtggct cctggccgtg accttcttgg 200

ttcccagagc tcagcccttg gcccctcaag actttgaaga agaggaggca 250
```

258

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gatgagactg agacggcgtg gccgcctttg ccggctgtcc cctgcgacta 300

cgaccactgc cgacacctgc aggtgccctg caaggagcta cagagggtcg 350

ggccggcggc ctgcctgtgc ccaggactct ccagccccgc ccagccgccc 400

gacccgccgc gcatgggaga agtgcgcatt gcggccgaag agggccgcgc 450

agtggtccac tggtgtgccc ccttctcccc ggtcctccac tactggctgc 500

tgctttggga cggcagcgag gctgcgcaga aggggccccc gctgaacgct 550

acggtccgca gagccgaact gaaggggctg aagccagggg gcatttatgt 600

cgtttgcgta gtggccgcta acgaggccgg ggcaagccgc gtgccccagg 650

ctggaggaga gggcctcgag ggggccgaca tccctgcctt cgggccttgc 700

agccgccttg cggtgccgcc caaccccgc actctggtcc acgcggccgt 750

cggggtgggc acggccctgg ccctgctaag ctgtgccgcc ctggtgtggc 800

acttctgcct gcgcgatcgc tggggctgcc cgcgccgagc cgccgcccga 850

gccgcagggg cgctctgaaa ggggcctggg ggcatctcgg gcacagacag 900

ccccacctgg ggcgctcagc ctggccccccg ggaaagagga aaacccgctg 950

cctccaggga gggctggacg gcgagctggg agccagcccc aggctccagg 1000

gccacggcgg agtcatggtt ctcaggactg agcgcttgtt taggtccggt 1050

acttggcgct ttgtttcctg gctgaggtct gggaaggaat agaaaggggc 1100

ccccaatttt tttttaagcg gccagataat aaataatgta acctttgcgg 1150

ttaaaaaaaa aaaaaaaaaa 1170
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<210> 271
<211> 238
<212> PRT
<213> Homo sapiens

<400> 271
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Met Leu Gly Ser Pro Cys Leu Leu Trp Leu Leu Ala Val Thr Phe
 1               5                  10                  15

Leu Val Pro Arg Ala Gln Pro Leu Ala Pro Gln Asp Phe Glu Glu
                20                  25                  30

Glu Glu Ala Asp Glu Thr Glu Thr Ala Trp Pro Pro Leu Pro Ala
                35                  40                  45

Val Pro Cys Asp Tyr Asp His Cys Arg His Leu Gln Val Pro Cys
                50                  55                  60

Lys Glu Leu Gln Arg Val Gly Pro Ala Ala Cys Leu Cys Pro Gly
                65                  70                  75
```

259

Leu Ser Ser Pro Ala Gln Pro Pro Asp Pro Pro Arg Met Gly Glu
           80   85   90

Val Arg Ile Ala Ala Glu Glu Gly Arg Ala Val Val His Trp Cys
           95   100   105

Ala Pro Phe Ser Pro Val Leu His Tyr Trp Leu Leu Leu Trp Asp
            110   115   120

Gly Ser Glu Ala Ala Gln Lys Gly Pro Pro Leu Asn Ala Thr Val
            125   130   135

Arg Arg Ala Glu Leu Lys Gly Leu Lys Pro Gly Gly Ile Tyr Val
            140   145   150

Val Cys Val Val Ala Ala Asn Glu Ala Gly Ala Ser Arg Val Pro
            155   160   165

Gln Ala Gly Gly Glu Gly Leu Glu Gly Ala Asp Ile Pro Ala Phe
            170   175   180

Gly Pro Cys Ser Arg Leu Ala Val Pro Pro Asn Pro Arg Thr Leu
            185   190   195

Val His Ala Ala Val Gly Val Gly Thr Ala Leu Ala Leu Leu Ser
            200   205   210

Cys Ala Ala Leu Val Trp His Phe Cys Leu Arg Asp Arg Trp Gly
            215   220   225

Cys Pro Arg Arg Ala Ala Ala Arg Ala Ala Gly Ala Leu
            230   235

<210> 272
<211> 2397
<212> DNA
<213> Homo sapiens

<400> 272
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cgaagaagtt ccctgccccg atgagccccc gccgtgcgtc cccgactatc 100

cccaggcggg cgtggggcac cgggcccagc gccgacgatc gctgccgttt 150

tgcccttggg agtaggatgt ggtgaaagga tggggcttct cccttacggg 200

gctcacaatg gccagagaag attccgtgaa gtgtctgcgc tgcctgctct 250

acgccctcaa tctgctcttt tggttaatgt ccatcagtgt gttggcagtt 300

tctgcttgga tgagggacta cctaaataat gttctcactt taactgcaga 350

aacgagggta gaggaagcag tcattttgac ttactttcct gtggttcatc 400

cggtcatgat tgctgtttgc tgtttcctta tcattgtggg gatgttagga 450

tattgtggaa cggtgaaaag aaatctgttg cttcttgcat ggtactttgg 500

aagtttgctt gtcattttct gtgtagaact ggcttgtggc gtttggacat 550

atgaacagga acttatggtt ccagtacaat ggtcagatat ggtcactttg 600

aaagccagga tgacaaatta tggattacct agatatcggt ggcttactca 650

tgcttggaat ttttttcaga gagagtttaa gtgctgtgga gtagtatatt 700

tcactgactg gttggaaatg acagagatgg actggccccc agattcctgc 750

tgtgttagag aattcccagg atgttccaaa caggcccacc aggaagatct 800

cagtgacctt tatcaagagg gttgtgggaa gaaaatgtat tcctttttga 850

gaggaaccaa acaactgcag gtgctgaggt ttctgggaat ctccattggg 900

gtgacacaaa tcctggccat gattctcacc attactctgc tctgggctct 950

gtattatgat agaagggagc ctgggacaga ccaaatgatg tccttgaaga 1000

atgacaactc tcagcacctg tcatgtccct cagtagaact gttgaaacca 1050

agcctgtcaa gaatctttga acacacatcc atggcaaaca gctttaatac 1100

acactttgag atggaggagt tataaaaaga aatgtcacag aagaaaacca 1150

caaacttgtt ttattggact tgtgaatttt tgagtacata ctatgtgttt 1200

cagaaatatg tagaaataaa aatgttgcca taaaataaca cctaagcata 1250

tactattcta tgctttaaaa tgaggatgga aaagtttcat gtcataagtc 1300

accacctgga caataattga tgcccttaaa atgctgaaga cagatgtcat 1350

acccactgtg tagcctgtgt atgactttta ctgaacacag ttatgttttg 1400

aggcagcatg gtttgattag catttccgca tccatgcaaa cgagtcacat 1450

atggtgggac tggagccata gtaaaggttg atttacttct accaactagt 1500

atataaagta ctaattaaat gctaacatag gaagttagaa aatactaata 1550

acttttatta ctcagcgatc tattcttctg atgctaaata aattatatat 1600

cagaaaactt tcaatattgg tgactaccta aatgtgattt ttgctggtta 1650

ctaaaatatt cttaccactt aaaagagcaa gctaacacat tgtcttaagc 1700

tgatcaggga ttttttgtat ataagtctgt gttaaatctg tataattcag 1750

tcgatttcag ttctgataat gttaagaata accattatga aaaggaaaat 1800

ttgtcctgta tagcatcatt attttttagcc tttcctgtta ataaagcttt 1850

actattctgt cctgggctta tattacacat ataactgtta tttaaatact 1900

taaccactaa ttttgaaaat taccagtgtg atacatagga atcattattc 1950

261

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agaatgtagt ctggtcttta ggaagtatta ataagaaaat ttgcacataa 2000

cttagttgat tcagaaagga cttgtatgct gttttttctcc caaatgaaga 2050

ctctttttga cactaaacac ttttttaaaaa gcttatcttt gccttctcca 2100

aacaagaagc aatagtctcc aagtcaatat aaattctaca gaaaatagtg 2150

ttcttttttct ccagaaaaat gcttgtgaga atcattaaaa catgtgacaa 2200

tttagagatt ctttgtttta tttcactgat taatatactg tggcaaatta 2250

cacagattat taaattttttt tacaagagta tagtatattt atttgaaatg 2300

ggaaaagtgc attttactgt atttttgtgta ttttgtttat ttctcagaat 2350

atggaaagaa aattaaaatg tgtcaataaa tattttctag agagtaa 2397
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<210> 273
<211> 305
<212> PRT
<213> Homo sapiens

<400> 273

```
Met Ala Arg Glu Asp Ser Val Lys Cys Leu Arg Cys Leu Leu Tyr
 1               5                  10                  15

Ala Leu Asn Leu Leu Phe Trp Leu Met Ser Ile Ser Val Leu Ala
            20                  25                  30

Val Ser Ala Trp Met Arg Asp Tyr Leu Asn Asn Val Leu Thr Leu
            35                  40                  45

Thr Ala Glu Thr Arg Val Glu Glu Ala Val Ile Leu Thr Tyr Phe
            50                  55                  60

Pro Val Val His Pro Val Met Ile Ala Val Cys Cys Phe Leu Ile
            65                  70                  75

Ile Val Gly Met Leu Gly Tyr Cys Gly Thr Val Lys Arg Asn Leu
            80                  85                  90

Leu Leu Leu Ala Trp Tyr Phe Gly Ser Leu Leu Val Ile Phe Cys
            95                 100                 105

Val Glu Leu Ala Cys Gly Val Trp Thr Tyr Glu Gln Glu Leu Met
           110                 115                 120

Val Pro Val Gln Trp Ser Asp Met Val Thr Leu Lys Ala Arg Met
           125                 130                 135

Thr Asn Tyr Gly Leu Pro Arg Tyr Arg Trp Leu Thr His Ala Trp
           140                 145                 150

Asn Phe Phe Gln Arg Glu Phe Lys Cys Cys Gly Val Val Tyr Phe
           155                 160                 165

Thr Asp Trp Leu Glu Met Thr Glu Met Asp Trp Pro Pro Asp Ser
```

262

```
                170                 175                 180
Cys Cys Val Arg Glu Phe Pro Gly Cys Ser Lys Gln Ala His Gln
                185                 190                 195
Glu Asp Leu Ser Asp Leu Tyr Gln Glu Gly Cys Gly Lys Lys Met
                200                 205                 210
Tyr Ser Phe Leu Arg Gly Thr Lys Gln Leu Gln Val Leu Arg Phe
                215                 220                 225
Leu Gly Ile Ser Ile Gly Val Thr Gln Ile Leu Ala Met Ile Leu
                230                 235                 240
Thr Ile Thr Leu Leu Trp Ala Leu Tyr Tyr Asp Arg Arg Glu Pro
                245                 250                 255
Gly Thr Asp Gln Met Met Ser Leu Lys Asn Asp Asn Ser Gln His
                260                 265                 270
Leu Ser Cys Pro Ser Val Glu Leu Leu Lys Pro Ser Leu Ser Arg
                275                 280                 285
Ile Phe Glu His Thr Ser Met Ala Asn Ser Phe Asn Thr His Phe
                290                 295                 300
Glu Met Glu Glu Leu
                305
```

<210> 274
<211> 2063
<212> DNA
<213> Homo sapiens

<400> 274
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gagagaggca gcagcttgct cagcggacaa ggatgctggg cgtgagggac  50
caaggcctgc cctgcactcg ggcctcctcc agccagtgct gaccagggac 100
ttctgacctg ctggccagcc aggacctgtg tggggaggcc ctcctgctgc 150
cttggggtga caatctcagc tccaggctac agggagaccg ggaggatcac 200
agagccagca tgttacagga tcctgacagt gatcaacctc tgaacagcct 250
cgatgtcaaa cccctgcgca aaccccgtat ccccatggag accttcagaa 300
aggtggggat ccccatcatc atagcactac tgagcctggc gagtatcatc 350
attgtggttg tcctcatcaa ggtgattctg gataaatact acttcctctg 400
cgggcagcct ctccacttca tcccgaggaa gcagctgtgt gacggagagc 450
tggactgtcc cttgggggag gacgaggagc actgtgtcaa gagcttcccc 500
gaagggcctg cagtggcagt ccgcctctcc aaggaccgat ccacactgca 550
ggtgctggac tcggccacag ggaactggtt ctctgcctgt ttcgacaact 600
```

263

```
tcacagaagc tctcgctgag acagcctgta ggcagatggg ctacagcaga 650

gctgtggaga ttggcccaga ccaggatctg gatgttgttg aaatcacaga 700

aaacagccag gagcttcgca tgcggaactc aagtgggccc tgtctctcag 750

gctccctggt ctccctgcac tgtcttgcct gtgggaagag cctgaagacc 800

ccccgtgtgg tgggtgggga ggaggcctct gtggattctt ggccttggca 850

ggtcagcatc cagtacgaca aacagcacgt ctgtggaggg agcatcctgg 900

accccactg ggtcctcacg gcagcccact gcttcaggaa acataccgat 950

gtgttcaact ggaaggtgcg ggcaggctca gacaaactgg gcagcttccc 1000

atccctggct gtggccaaga tcatcatcat tgaattcaac cccatgtacc 1050

ccaaagacaa tgacatcgcc ctcatgaagc tgcagttccc actcactttc 1100

tcaggcacag tcaggcccat ctgtctgccc ttctttgatg aggagctcac 1150

tccagccacc ccactctgga tcattggatg gggctttacg aagcagaatg 1200

gagggaagat gtctgacata ctgctgcagg cgtcagtcca ggtcattgac 1250

agcacacggt gcaatgcaga cgatgcgtac caggggaag tcaccgagaa 1300

gatgatgtgt gcaggcatcc cggaagggg tgtggacacc tgccagggtg 1350

acagtggtgg gccctgatg taccaatctg accagtggca tgtggtgggc 1400

atcgttagct ggggctatgg ctgcggggc ccgagcaccc caggagtata 1450

caccaaggtc tcagcctatc tcaactggat ctacaatgtc tggaaggctg 1500

agctgtaatg ctgctgcccc tttgcagtgc tgggagccgc ttccttcctg 1550

ccctgcccac ctggggatcc cccaaagtca gacacagagc aagagtcccc 1600

ttgggtacac ccctctgccc acagcctcag catttcttgg agcagcaaag 1650

ggcctcaatt cctgtaagag accctcgcag cccagaggcg cccagaggaa 1700

gtcagcagcc ctagctcggc cacacttggt gctcccagca tcccagggag 1750

agacacagcc cactgaacaa ggtctcaggg gtattgctaa gccaagaagg 1800

aactttccca cactactgaa tggaagcagg ctgtcttgta aaagcccaga 1850

tcactgtggg ctggagagga gaaggaaagg gtctgcgcca gccctgtccg 1900

tcttcacccа tccccaagcc tactagagca agaaaccagt tgtaatataa 1950

aatgcactgc cctactgttg gtatgactac cgttacctac tgttgtcatt 2000

gttattacag ctatggccac tattattaaa gagctgtgta acatctctgg 2050
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264

caaaaaaaaa aaa 2063

<210> 275
<211> 432
<212> PRT
<213> Homo sapiens

<400> 275

```
Met Leu Gln Asp Pro Asp Ser Asp Gln Pro Leu Asn Ser Leu Asp
 1               5                  10                  15

Val Lys Pro Leu Arg Lys Pro Arg Ile Pro Met Glu Thr Phe Arg
                20                  25                  30

Lys Val Gly Ile Pro Ile Ile Ile Ala Leu Leu Ser Leu Ala Ser
                35                  40                  45

Ile Ile Ile Val Val Val Leu Ile Lys Val Ile Leu Asp Lys Tyr
                50                  55                  60

Tyr Phe Leu Cys Gly Gln Pro Leu His Phe Ile Pro Arg Lys Gln
                65                  70                  75

Leu Cys Asp Gly Glu Leu Asp Cys Pro Leu Gly Glu Asp Glu Glu
                80                  85                  90

His Cys Val Lys Ser Phe Pro Glu Gly Pro Ala Val Ala Val Arg
                95                  100                 105

Leu Ser Lys Asp Arg Ser Thr Leu Gln Val Leu Asp Ser Ala Thr
                110                 115                 120

Gly Asn Trp Phe Ser Ala Cys Phe Asp Asn Phe Thr Glu Ala Leu
                125                 130                 135

Ala Glu Thr Ala Cys Arg Gln Met Gly Tyr Ser Arg Ala Val Glu
                140                 145                 150

Ile Gly Pro Asp Gln Asp Leu Asp Val Val Glu Ile Thr Glu Asn
                155                 160                 165

Ser Gln Glu Leu Arg Met Arg Asn Ser Ser Gly Pro Cys Leu Ser
                170                 175                 180

Gly Ser Leu Val Ser Leu His Cys Leu Ala Cys Gly Lys Ser Leu
                185                 190                 195

Lys Thr Pro Arg Val Val Gly Gly Glu Glu Ala Ser Val Asp Ser
                200                 205                 210

Trp Pro Trp Gln Val Ser Ile Gln Tyr Asp Lys Gln His Val Cys
                215                 220                 225

Gly Gly Ser Ile Leu Asp Pro His Trp Val Leu Thr Ala Ala His
                230                 235                 240

Cys Phe Arg Lys His Thr Asp Val Phe Asn Trp Lys Val Arg Ala
                245                 250                 255
```

265

```
Gly Ser Asp Lys Leu Gly Ser Phe Pro Ser Leu Ala Val Ala Lys
            260             265                         270

Ile Ile Ile Ile Glu Phe Asn Pro Met Tyr Pro Lys Asp Asn Asp
            275             280                         285

Ile Ala Leu Met Lys Leu Gln Phe Pro Leu Thr Phe Ser Gly Thr
            290             295                         300

Val Arg Pro Ile Cys Leu Pro Phe Phe Asp Glu Glu Leu Thr Pro
            305             310                         315

Ala Thr Pro Leu Trp Ile Ile Gly Trp Gly Phe Thr Lys Gln Asn
            320             325                         330

Gly Gly Lys Met Ser Asp Ile Leu Leu Gln Ala Ser Val Gln Val
            335             340                         345

Ile Asp Ser Thr Arg Cys Asn Ala Asp Asp Ala Tyr Gln Gly Glu
            350             355                         360

Val Thr Glu Lys Met Met Cys Ala Gly Ile Pro Glu Gly Gly Val
            365             370                         375

Asp Thr Cys Gln Gly Asp Ser Gly Gly Pro Leu Met Tyr Gln Ser
            380             385                         390

Asp Gln Trp His Val Val Gly Ile Val Ser Trp Gly Tyr Gly Cys
            395             400                         405

Gly Gly Pro Ser Thr Pro Gly Val Tyr Thr Lys Val Ser Ala Tyr
            410             415                         420

Leu Asn Trp Ile Tyr Asn Val Trp Lys Ala Glu Leu
            425             430
```

<210> 276
<211> 3143
<212> DNA
<213> Homo sapiens

<400> 276
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gggctgaggc actgagagac cggaaagcct ggcattccag agggagggaa 50

acgcagcggc atccccaggc tccagagctc cctggtgaca gtctgtggct 100

gagcatggcc ctcccagccc tgggcctgga cccctggagc ctcctgggcc 150

ttttcctctt ccaactgctt cagctgctgc tgccgacgac gaccgcgggg 200

ggaggcgggc aggggcccat gcccagggtc agatactatg caggggatga 250

acgtagggca cttagcttct tccaccagaa gggcctccag gattttgaca 300

ctctgctcct gagtggtgat ggaaatactc tctacgtggg ggctcgagaa 350

gccattctgg ccttggatat ccaggatcca ggggtcccca ggctaaagaa 400
```

266

```
catgataccg tggccagcca gtgacagaaa aaagagtgaa tgtgccttta 450

agaagaagag caatgagaca cagtgtttca acttcatccg tgtcctggtt 500

tcttacaatg tcacccatct ctacacctgc ggcaccttcg ccttcagccc 550

tgcttgtacc ttcattgaac ttcaagattc ctacctgttg cccatctcgg 600

aggacaaggt catggaggga aaaggccaaa gcccctttga ccccgctcac 650

aagcatacgg ctgtcttggt ggatgggatg ctctattctg gtactatgaa 700

caacttcctg ggcagtgagc ccatcctgat gcgcacactg ggatcccagc 750

ctgtcctcaa gaccgacaac ttcctccgct ggctgcatca tgacgcctcc 800

tttgtggcag ccatcccttc gacccaggtc gtctacttct tcttcgagga 850

gacagccagc gagtttgact tctttgagag gctccacaca tcgcgggtgg 900

ctagagtctg caagaatgac gtgggcggcg aaaagctgct gcagaagaag 950

tggaccacct tcctgaaggc ccagctgctc tgcacccagc cggggcagct 1000

gcccttcaac gtcatccgcc acgcggtcct gctccccgcc gattctccca 1050

cagctcccca catctacgca gtcttcacct cccagtggca ggttggcggg 1100

accaggagct ctgcggtttg tgccttctct ctcttggaca ttgaacgtgt 1150

ctttaagggg aaatacaaag agttgaacaa agaaacttca cgctggacta 1200

cttatagggg ccctgagacc aaccccggc caggcagttg ctcagtgggc 1250

ccctcctctg ataaggccct gaccttcatg aaggaccatt tcctgatgga 1300

tgagcaagtg gtggggacgc ccctgctggt gaaatctggc gtggagtata 1350

cacggcttgc agtggagaca gcccagggcc ttgatgggca cagccatctt 1400

gtcatgtacc tgggaaccac cacagggtcg ctccacaagg ctgtggtaag 1450

tggggacagc agtgctcatc tggtggaaga gattcagctg ttccctgacc 1500

ctgaacctgt tcgcaacctg cagctggccc ccacccaggg tgcagtgttt 1550

gtaggcttct caggaggtgt ctggagggtg ccccgagcca actgtagtgt 1600

ctatgagagc tgtgtggact gtgtccttgc ccgggacccc cactgtgcct 1650

gggaccctga gtcccgaacc tgttgcctcc tgtctgcccc caacctgaac 1700

tcctggaagc aggacatgga gcgggggaac ccagagtggg catgtgccag 1750

tggcccccatg agcaggagcc ttcggcctca gagccgcccg caaatcatta 1800

aagaagtcct ggctgtcccc aactccatcc tggagctccc ctgcccccac 1850
```

267

```
ctgtcagcct tggcctctta ttattggagt catggcccag cagcagtccc 1900

agaagcctct tccactgtct acaatggctc cctcttgctg atagtgcagg 1950

atggagttgg gggtctctac cagtgctggg caactgagaa tggcttttca 2000

taccctgtga tctcctactg ggtggacagc caggaccaga ccctggccct 2050

ggatcctgaa ctggcaggca tcccccggga gcatgtgaag gtcccgttga 2100

ccagggtcag tggtggggcc gccctggctg cccagcagtc ctactggccc 2150

cactttgtca ctgtcactgt cctctttgcc ttagtgcttt caggagccct 2200

catcatcctc gtggcctccc cattgagagc actccgggct cggggcaagg 2250

ttcagggctg tgagaccctg cgccctgggg agaaggcccc gttaagcaga 2300

gagcaacacc tccagtctcc caaggaatgc aggacctctg ccagtgatgt 2350

ggacgctgac aacaactgcc taggcactga ggtagcttaa actctaggca 2400

caggccgggg ctgcggtgca ggcacctggc catgctggct gggcggccca 2450

agcacagccc tgactaggat dacagcagca caaaagacca cctttctccc 2500

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agctctctaa cagggtgggg gctaccccca gacctgctcc tacactgata 2650

ttgaagaacc tggagaggat ccttcagttc tggccattcc agggaccctc 2700

cagaaacaca gtgtttcaag agaccctaaa aaacctgcct gtcccaggac 2750

cctatggtaa tgaacaccaa acatctaaac aatcatatgc taacatgcca 2800

ctcctggaaa ctccactctg aagctgccgc tttggacacc aacactccct 2850

tctcccaggg tcatgcaggg atctgctccc tcctgcttcc cttaccagtc 2900

gtgcaccgct gactcccagg aagtctttcc tgaagtctga ccacctttct 2950

tcttgcttca gttggggcag actctgatcc cttctgccct ggcagaatgg 3000

caggggtaat ctgagccttc ttcactcctt taccctagct gacccccttca 3050

cctctccccc tcccttttcc tttgttttgg gattcagaaa actgcttgtc 3100

agagactgtt tattttttat taaaaatata aggcttaaaa aaa 3143
```

<210> 277
<211> 761
<212> PRT
<213> Homo sapiens

<400> 277

```
Met Ala Leu Pro Ala Leu Gly Leu Asp Pro Trp Ser Leu Leu Gly
 1               5                  10                      15

Leu Phe Leu Phe Gln Leu Leu Gln Leu Leu Leu Pro Thr Thr Thr
                20                  25                      30

Ala Gly Gly Gly Gly Gln Gly Pro Met Pro Arg Val Arg Tyr Tyr
                35                  40                      45

Ala Gly Asp Glu Arg Arg Ala Leu Ser Phe Phe His Gln Lys Gly
                50                  55                      60

Leu Gln Asp Phe Asp Thr Leu Leu Leu Ser Gly Asp Gly Asn Thr
                65                  70                      75

Leu Tyr Val Gly Ala Arg Glu Ala Ile Leu Ala Leu Asp Ile Gln
                80                  85                      90

Asp Pro Gly Val Pro Arg Leu Lys Asn Met Ile Pro Trp Pro Ala
                95                  100                     105

Ser Asp Arg Lys Lys Ser Glu Cys Ala Phe Lys Lys Lys Ser Asn
                110                 115                     120

Glu Thr Gln Cys Phe Asn Phe Ile Arg Val Leu Val Ser Tyr Asn
                125                 130                     135

Val Thr His Leu Tyr Thr Cys Gly Thr Phe Ala Phe Ser Pro Ala
                140                 145                     150

Cys Thr Phe Ile Glu Leu Gln Asp Ser Tyr Leu Leu Pro Ile Ser
                155                 160                     165

Glu Asp Lys Val Met Glu Gly Lys Gly Gln Ser Pro Phe Asp Pro
                170                 175                     180

Ala His Lys His Thr Ala Val Leu Val Asp Gly Met Leu Tyr Ser
                185                 190                     195

Gly Thr Met Asn Asn Phe Leu Gly Ser Glu Pro Ile Leu Met Arg
                200                 205                     210

Thr Leu Gly Ser Gln Pro Val Leu Lys Thr Asp Asn Phe Leu Arg
                215                 220                     225

Trp Leu His His Asp Ala Ser Phe Val Ala Ala Ile Pro Ser Thr
                230                 235                     240

Gln Val Val Tyr Phe Phe Phe Glu Glu Thr Ala Ser Glu Phe Asp
                245                 250                     255

Phe Phe Glu Arg Leu His Thr Ser Arg Val Ala Arg Val Cys Lys
                260                 265                     270

Asn Asp Val Gly Gly Glu Lys Leu Leu Gln Lys Lys Trp Thr Thr
                275                 280                     285

Phe Leu Lys Ala Gln Leu Leu Cys Thr Gln Pro Gly Gln Leu Pro
```

269

```
                    290                     295                     300
Phe Asn Val Ile Arg His Ala Val Leu Leu Pro Ala Asp Ser Pro
                305                     310                     315
Thr Ala Pro His Ile Tyr Ala Val Phe Thr Ser Gln Trp Gln Val
                320                     325                     330
Gly Gly Thr Arg Ser Ser Ala Val Cys Ala Phe Ser Leu Leu Asp
                335                     340                     345
Ile Glu Arg Val Phe Lys Gly Lys Tyr Lys Glu Leu Asn Lys Glu
                350                     355                     360
Thr Ser Arg Trp Thr Thr Tyr Arg Gly Pro Glu Thr Asn Pro Arg
                365                     370                     375
Pro Gly Ser Cys Ser Val Gly Pro Ser Ser Asp Lys Ala Leu Thr
                380                     385                     390
Phe Met Lys Asp His Phe Leu Met Asp Glu Gln Val Val Gly Thr
                395                     400                     405
Pro Leu Leu Val Lys Ser Gly Val Glu Tyr Thr Arg Leu Ala Val
                410                     415                     420
Glu Thr Ala Gln Gly Leu Asp Gly His Ser His Leu Val Met Tyr
                425                     430                     435
Leu Gly Thr Thr Thr Gly Ser Leu His Lys Ala Val Val Ser Gly
                440                     445                     450
Asp Ser Ser Ala His Leu Val Glu Glu Ile Gln Leu Phe Pro Asp
                455                     460                     465
Pro Glu Pro Val Arg Asn Leu Gln Leu Ala Pro Thr Gln Gly Ala
                470                     475                     480
Val Phe Val Gly Phe Ser Gly Gly Val Trp Arg Val Pro Arg Ala
                485                     490                     495
Asn Cys Ser Val Tyr Glu Ser Cys Val Asp Cys Val Leu Ala Arg
                500                     505                     510
Asp Pro His Cys Ala Trp Asp Pro Glu Ser Arg Thr Cys Cys Leu
                515                     520                     525
Leu Ser Ala Pro Asn Leu Asn Ser Trp Lys Gln Asp Met Glu Arg
                530                     535                     540
Gly Asn Pro Glu Trp Ala Cys Ala Ser Gly Pro Met Ser Arg Ser
                545                     550                     555
Leu Arg Pro Gln Ser Arg Pro Gln Ile Ile Lys Glu Val Leu Ala
                560                     565                     570
Val Pro Asn Ser Ile Leu Glu Leu Pro Cys Pro His Leu Ser Ala
                575                     580                     585
```

270

```
Leu Ala Ser Tyr Tyr Trp Ser His Gly Pro Ala Ala Val Pro Glu
              590                 595                 600

Ala Ser Ser Thr Val Tyr Asn Gly Ser Leu Leu Leu Ile Val Gln
              605                 610                 615

Asp Gly Val Gly Gly Leu Tyr Gln Cys Trp Ala Thr Glu Asn Gly
              620                 625                 630

Phe Ser Tyr Pro Val Ile Ser Tyr Trp Val Asp Ser Gln Asp Gln
              635                 640                 645

Thr Leu Ala Leu Asp Pro Glu Leu Ala Gly Ile Pro Arg Glu His
              650                 655                 660

Val Lys Val Pro Leu Thr Arg Val Ser Gly Gly Ala Ala Leu Ala
              665                 670                 675

Ala Gln Gln Ser Tyr Trp Pro His Phe Val Thr Val Thr Val Leu
              680                 685                 690

Phe Ala Leu Val Leu Ser Gly Ala Leu Ile Ile Leu Val Ala Ser
              695                 700                 705

Pro Leu Arg Ala Leu Arg Ala Arg Gly Lys Val Gln Gly Cys Glu
              710                 715                 720

Thr Leu Arg Pro Gly Glu Lys Ala Pro Leu Ser Arg Glu Gln His
              725                 730                 735

Leu Gln Ser Pro Lys Glu Cys Arg Thr Ser Ala Ser Asp Val Asp
              740                 745                 750

Ala Asp Asn Asn Cys Leu Gly Thr Glu Val Ala
              755                 760


<210> 278
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 278
 ctgctggtga aatctggcgt ggag        24

<210> 279
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.
```

<400> 279
gtctggtcct ggctgtccac ccag 24

<210> 280
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 280
catcttgtca tgtacctggg aaccaccaca gggtcgctcc acaag 45

<210> 281
<211> 2320
<212> DNA
<213> Homo sapiens

<400> 281
agggtccctt agccgggcgc agggcgcgca gcccaggctg agatccgcgg 50

cttccgtaga agtgagcatg gctgggcagc gagtgcttct tctagtgggc 100

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atctacagta ggtggaagcc attatctact gatggaccgg gtttctcaga 200

ttcttcaaga tcacggtcat aatgtcacca tgcttaacca caaaagaggt 250

ccttttatgc cagattttaa aaaggaagaa aaatcatatc aagttatcag 300

ttggcttgca cctgaagatc atcaaagaga atttaaaaag agttttgatt 350

tctttctgga agaaacttta ggtggcagag gaaaatttga aaacttatta 400

aatgttctag aatacttggc gttgcagtgc agtcattttt taaatagaaa 450

ggatatcatg gattccttaa agaatgagaa cttcgacatg gtgatagttg 500

aaacttttga ctactgtcct ttcctgattg ctgagaagct tgggaagcca 550

tttgtggcca ttctttccac ttcattcggc tctttggaat ttgggctacc 600

aatccccttg tcttatgttc cagtattccg ttccttgctg actgatcaca 650

tggacttctg gggccgagtg aagaattttc tgatgttctt tagtttctgc 700

aggaggcaac agcacatgca gtctacattt gacaacacca tcaaggaaca 750

tttcacagaa ggctctaggc cagttttgtc tcatcttcta ctgaaagcag 800

agttgtggtt cattaactct gactttgcct ttgattttgc tcgacctctg 850

cttcccaaca ctgtttatgt tggaggcttg atggaaaaac ctattaaacc 900

272

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agtaccacaa gacttggaga acttcattgc caagtttggg gactctggtt 950

ttgtccttgt gaccttgggc tccatggtga acacctgtca gaatccggaa 1000

atcttcaagg agatgaacaa tgcctttgct cacctacccc aaggggtgat 1050

atggaagtgt cagtgttctc attggcccaa agatgtccac ctggctgcaa 1100

atgtgaaaat tgtggactgg cttcctcaga gtgacctcct ggctcaccca 1150

agcatccgtc tgtttgtcac ccacggcggg cagaatagca taatggaggc 1200

catccagcat ggtgtgccca tggtggggat ccctctcttt ggagaccagc 1250

ctgaaaacat ggtccgagta gaagccaaaa agtttggtgt ttctattcag 1300

ttaaagaagc tcaaggcaga gacattggct cttaagatga aacaaatcat 1350

ggaagacaag agatacaagt ccgcggcagt ggctgccagt gtcatcctgc 1400

gctcccaccc gctcagcccc acacagcggc tggtgggctg gattgaccac 1450

gtcctccaga caggggggcgc gacgcacctc aagccctatg tctttcagca 1500

gccctggcat gagcagtacc tgttcgacgt ttttgtgttt ctgctggggc 1550

tcactctggg gactctatgg ctttgtggga agctgctggg catggctgtc 1600

tggtggctgc gtggggccag aaaggtgaag gagacataag gccaggtgca 1650

gccttggcgg ggtctgtttg gtgggcgatg tcaccatttc tagggagctt 1700

cccactagtt ctggcagccc cattctctag tccttctagt tatctcctgt 1750

tttcttgaag aacaggaaaa atggccaaaa atcatccttt ccacttgcta 1800

attttgctac aaattcatcc ttactagctc ctgcctgcta gcagaaatct 1850

ttccagtcct cttgtcctcc tttgtttgcc atcagcaagg gctatgctgt 1900

gattctgtct ctgagtgact tggaccactg accctcagat ttccagcctt 1950

aaaatccacc ttccttctca tgcgcctctc cgaatcacac cctgactctt 2000

ccagcctcca tgtccagacc tagtcagcct ctctcactcc tgcccctact 2050

atctatcatg gaataacatc caagaaagac accttgcata ttctttcagt 2100

ttctgttttg ttctcccaca tattctcttc aatgctcagg aagcctgccc 2150

tgtgcttgag agttcagggc cggacacagg ctcacaggtc tccacattgg 2200

gtccctgtct ctggtgccca cagtgagctc cttcttggct gagcaggcat 2250

ggagactgta ggtttccaga tttcctgaaa aataaaagtt tacagcgtta 2300

tctctcccca acctcactaa 2320
```

273

.

<210> 282
<211> 523
<212> PRT
<213> Homo sapiens

<400> 282

```
Met Ala Gly Gln Arg Val Leu Leu Leu Val Gly Phe Leu Leu Pro
  1               5                  10                  15

Gly Val Leu Leu Ser Glu Ala Ala Lys Ile Leu Thr Ile Ser Thr
                 20                  25                  30

Val Gly Gly Ser His Tyr Leu Leu Met Asp Arg Val Ser Gln Ile
                 35                  40                  45

Leu Gln Asp His Gly His Asn Val Thr Met Leu Asn His Lys Arg
                 50                  55                  60

Gly Pro Phe Met Pro Asp Phe Lys Lys Glu Glu Lys Ser Tyr Gln
                 65                  70                  75

Val Ile Ser Trp Leu Ala Pro Glu Asp His Gln Arg Glu Phe Lys
                 80                  85                  90

Lys Ser Phe Asp Phe Phe Leu Glu Glu Thr Leu Gly Gly Arg Gly
                 95                 100                 105

Lys Phe Glu Asn Leu Leu Asn Val Leu Glu Tyr Leu Ala Leu Gln
                110                 115                 120

Cys Ser His Phe Leu Asn Arg Lys Asp Ile Met Asp Ser Leu Lys
                125                 130                 135

Asn Glu Asn Phe Asp Met Val Ile Val Glu Thr Phe Asp Tyr Cys
                140                 145                 150

Pro Phe Leu Ile Ala Glu Lys Leu Gly Lys Pro Phe Val Ala Ile
                155                 160                 165

Leu Ser Thr Ser Phe Gly Ser Leu Glu Phe Gly Leu Pro Ile Pro
                170                 175                 180

Leu Ser Tyr Val Pro Val Phe Arg Ser Leu Leu Thr Asp His Met
                185                 190                 195

Asp Phe Trp Gly Arg Val Lys Asn Phe Leu Met Phe Phe Ser Phe
                200                 205                 210

Cys Arg Arg Gln Gln His Met Gln Ser Thr Phe Asp Asn Thr Ile
                215                 220                 225

Lys Glu His Phe Thr Glu Gly Ser Arg Pro Val Leu Ser His Leu
                230                 235                 240

Leu Leu Lys Ala Glu Leu Trp Phe Ile Asn Ser Asp Phe Ala Phe
                245                 250                 255

Asp Phe Ala Arg Pro Leu Leu Pro Asn Thr Val Tyr Val Gly Gly
```

274

Leu Met Glu Lys Pro Ile Lys Pro Val Pro Gln Asp Leu Glu Asn
                275   280   285

Phe Ile Ala Lys Phe Gly Asp Ser Gly Phe Val Leu Val Thr Leu
                290   295   300

Gly Ser Met Val Asn Thr Cys Gln Asn Pro Glu Ile Phe Lys Glu
                305   310   315

Met Asn Asn Ala Phe Ala His Leu Pro Gln Gly Val Ile Trp Lys
                320   325   330

Cys Gln Cys Ser His Trp Pro Lys Asp Val His Leu Ala Ala Asn
                335   340   345

Val Lys Ile Val Asp Trp Leu Pro Gln Ser Asp Leu Leu Ala His
                350   355   360

Pro Ser Ile Arg Leu Phe Val Thr His Gly Gly Gln Asn Ser Ile
                365   370   375

Met Glu Ala Ile Gln His Gly Val Pro Met Val Gly Ile Pro Leu
                380   385   390

Phe Gly Asp Gln Pro Glu Asn Met Val Arg Val Glu Ala Lys Lys
                395   400   405

Phe Gly Val Ser Ile Gln Leu Lys Lys Leu Lys Ala Glu Thr Leu
                410   415   420

Ala Leu Lys Met Lys Gln Ile Met Glu Asp Lys Arg Tyr Lys Ser
                425   430   435

Ala Ala Val Ala Ala Ser Val Ile Leu Arg Ser His Pro Leu Ser
                440   445   450

Pro Thr Gln Arg Leu Val Gly Trp Ile Asp His Val Leu Gln Thr
                455   460   465

Gly Gly Ala Thr His Leu Lys Pro Tyr Val Phe Gln Gln Pro Trp
                470   475   480

His Glu Gln Tyr Leu Phe Asp Val Phe Val Phe Leu Leu Gly Leu
                485   490   495

Thr Leu Gly Thr Leu Trp Leu Cys Gly Lys Leu Leu Gly Met Ala
                500   505   510

Val Trp Trp Leu Arg Gly Ala Arg Lys Val Lys Glu Thr
                515   520

<210> 283
<211> 24
<212> DNA
<213> Artificial

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<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 283
 tgcctttgct cacctacccc aagg 24

<210> 284
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 284
 tcaggctggt ctccaaagag aggg 24

<210> 285
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 285
 cccaaagatg tccacctggc tgcaaatgtg aaaattgtgg actgg 45

<210> 286
<211> 2340
<212> DNA
<213> Homo sapiens

<400> 286
 gggctgttga tttgtggggg attttgaaga gaggaggaat aggaggaagg 50

 ggttgagggg ctgcctctgg catatgcaca cactcacaca ttctgtcaca 100

 cccgtcacac acacatacca tgttctccat cccccccaggt ccagccctca 150

 gtgctgtccc atccagcagg gctaccctga agctctggct gcagccctcc 200

 cgtccagtgg gcaggcggct tcatccctcc tttctctccc aaagcccaac 250

 tgctgtcact gcatgctctg ccaaggagga gggaactgca gtgacagcag 300

 gagtaagagt gggaggcagg acagagctgg gacacaggta tggagagggg 350

 gttcagcgag cctagagagg gcagactatc agggtgccgg cggtgagaat 400

 ccagggagag gagcggaaac agaagagggg cagaagaccg gggcacttgt 450
```

276

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gggttgcaga gcccctcagc catgttggga gccaagccac actggctacc  500

aggtcccta cacagtcccg ggctgccctt ggttctggtg cttctggccc  550

tggggggccgg gtgggcccag gagggggtcag agcccgtcct gctggagggg  600

gagtgcctgg tggtctgtga gcctggccga gctgctgcag ggggggcccgg  650

gggagcagcc ctgggagagg cacccctgg gcgagtggca tttgctgcgg  700

tccgaagcca ccaccatgag ccagcagggg aaaccggcaa tggcaccagt  750

ggggccatct acttcgacca ggtcctggtg aacgagggcg gtggctttga  800

ccgggcctct ggctccttcg tagcccctgt ccggggtgtc tacagcttcc  850

ggttccatgt ggtgaaggtg tacaaccgcc aaactgtcca ggtgagcctg  900

atgctgaaca cgtggcctgt catctcagcc tttgccaatg atcctgacgt  950

gacccgggag gcagccacca gctctgtgct actgcccttg gaccctgggg 1000

accgagtgtc tctgcgcctg cgtcggggga atctactggg tggttggaaa 1050

tactcaagtt tctctggctt cctcatcttc cctctctgag acccaagtc 1100

tttcaagcac aagaatccag cccctgacaa ctttcttctg ccctctcttg 1150

ccccagaaac agcagaggca ggagagagac tccctctggc tcctatccca 1200

cctctttgca tgggaccctg tgccaaacac ccaagtttaa gagaagagta 1250

gagctgtggc atctccagac caggcctttc cacccaccca ccccagtta 1300

ccctcccagc cacctgctgc atctgttcct gcctgcagcc ctaggatcag 1350

ggcaaggttt ggcaagaagg aagatctgca ctactttgcg gcctctgctc 1400

ctccggttcc cccaccccag cttcctgctc aatgctgatc agggacaggt 1450

ggcgcaggtg agcctgacag gccccacag gagcccagat ggacaagcct 1500

cagcgtaccc tgcaggcttc ttcctgtgag gaaagccagc atcacggatc 1550

tcagccagca ccgtcagaag ctgagccagc accgtatggg ctagggtggg 1600

aggctcagcc acaggcagaa gggtgggaag ggcctggagt ctgtggctgg 1650

tgaggaagga aggagggtgt attgtctaga ctgaacatgg tacacattct 1700

gcatgtatag cagagcagcc agcaggtagc aatcctggct gtccttctat 1750

gctggatccc agatggactc tggcccttac ctccccacct gagattaggg 1800

tgagtgtgtt tgctctggct gagagcagag ctgagagcag gtatacagag 1850

ctggaagtgg accatggaaa acatcgataa ccatgcatcc tcttgcttgg 1900
```

277

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ccacctcctg aaactgctcc acctttgaag tttgaacttt agtccctcca 1950

cactctgact gctgcctcct tcctcccagc tctctcactg agttatcttc 2000

actgtacctg ttccagcata tccccactat ctctctttct cctgatctgt 2050

gctgtcttat tctcctcctt aggcttccta ttacctggga ttccatgatt 2100

cattccttca gaccctctcc tgccagtatg ctaaaccctc cctctctctt 2150

tcttatcccg ctgtcccatt ggcccagcct ggatgaatct atcaataaaa 2200

caactagaga atggtggtca gtgagacact atagaattac taaggagaag 2250

atgcctctgg agtttggatc gggtgttaca ggtacaagta ggtatgttgc 2300

agaggaaaat aaatatcaaa ctgtatacta aaattaaaaa 2340
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<210> 287
<211> 205
<212> PRT
<213> Homo sapiens

<400> 287
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Met Leu Gly Ala Lys Pro His Trp Leu Pro Gly Pro Leu His Ser
1               5                   10                  15

Pro Gly Leu Pro Leu Val Leu Val Leu Leu Ala Leu Gly Ala Gly
                20                  25                  30

Trp Ala Gln Glu Gly Ser Glu Pro Val Leu Leu Glu Gly Glu Cys
                35                  40                  45

Leu Val Val Cys Glu Pro Gly Arg Ala Ala Ala Gly Gly Pro Gly
                50                  55                  60

Gly Ala Ala Leu Gly Glu Ala Pro Pro Gly Arg Val Ala Phe Ala
                65                  70                  75

Ala Val Arg Ser His His His Glu Pro Ala Gly Glu Thr Gly Asn
                80                  85                  90

Gly Thr Ser Gly Ala Ile Tyr Phe Asp Gln Val Leu Val Asn Glu
                95                  100                 105

Gly Gly Gly Phe Asp Arg Ala Ser Gly Ser Phe Val Ala Pro Val
                110                 115                 120

Arg Gly Val Tyr Ser Phe Arg Phe His Val Val Lys Val Tyr Asn
                125                 130                 135

Arg Gln Thr Val Gln Val Ser Leu Met Leu Asn Thr Trp Pro Val
                140                 145                 150

Ile Ser Ala Phe Ala Asn Asp Pro Asp Val Thr Arg Glu Ala Ala
                155                 160                 165

Thr Ser Ser Val Leu Leu Pro Leu Asp Pro Gly Asp Arg Val Ser
```

278

    Leu Arg Leu Arg Arg Gly Asn Leu Leu Gly Gly Trp Lys Tyr Ser
                185   190   195

    Ser Phe Ser Gly Phe Leu Ile Phe Pro Leu
                200   205

<210> 288
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 288
 aggcagccac cagctctgtg ctac 24

<210> 289
<211> 27
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-27
<223> Synthetic construct.

<400> 289
 cagagaggga agatgaggaa gccagag 27

<210> 290
<211> 42
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-42
<223> Synthetic construct.

<400> 290
 ctgtgctact gcccttggac cctggggacc gagtgtctct gc 42

<210> 291
<211> 1570
<212> DNA
<213> Homo sapiens

<400> 291
 gctgtttctc tcgcgccacc actggccgcc ggccgcagct ccaggtgtcc 50

 tagccgccca gcctcgacgc cgtcccggga cccctgtgct ctgcgcgaag 100

 ccctggcccc ggggggccggg gcatgggcca ggggcgcggg gtgaagcggc 150

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ttcccgcggg gccgtgactg ggcgggcttc agccatgaag accctcatag 200

ccgcctactc cggggtcctg cgcggcgagc gtcaggccga ggctgaccgg 250

agccagcgct ctcacggagg acctgcgctg tcgcgcgagg ggtctgggag 300

atggggcact ggatccagca tcctctccgc cctccaggac ctcttctctg 350

tcacctggct caataggtcc aaggtggaaa agcagctaca ggtcatctca 400

gtgctccagt gggtcctgtc cttccttgta ctgggagtgg cctgcagtgc 450

catcctcatg tacatattct gcactgattg ctggctcatc gctgtgctct 500

acttcacttg gctggtgttt gactggaaca cacccaagaa aggtggcagg 550

aggtcacagt gggtccgaaa ctgggctgtg tggcgctact ttcgagacta 600

ctttcccatc cagctggtga agacacacaa cctgctgacc accaggaact 650

atatctttgg ataccacccc catggtatca tgggcctggg tgccttctgc 700

aacttcagca cagaggccac agaagtgagc aagaagttcc caggcatacg 750

gccttacctg gctacactgg caggcaactt ccgaatgcct gtgttgaggg 800

agtacctgat gtctggaggt atctgccctg tcagccggga caccatagac 850

tatttgcttt caaagaatgg gagtggcaat gctatcatca tcgtggtcgg 900

gggtgcggct gagtctctga gctccatgcc tggcaagaat gcagtcaccc 950

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acattggttt cgccccatgc atcttccatg gtcgaggcct cttctcctcc 1150

gacacctggg ggctggtgcc ctactccaag cccatcacca ctgttgtggg 1200

agagcccatc accatcccca agctggagca cccaacccag caagacatcg 1250

acctgtacca caccatgtac atggaggccc tggtgaagct cttcgacaag 1300

cacaagacca agttcggcct cccggagact gaggtcctgg aggtgaactg 1350

agccagcctt cggggccaat tccctggagg aaccagctgc aaatcacttt 1400

tttgctctgt aaatttggaa gtgtcatggg tgtctgtggg ttatttaaaa 1450

gaaattataa caattttgct aaaccaaaaa aaaaaaaaa aaaaaaaaa 1500

aaaaaaaaa aaaaaaaaa aaaaaaaaa aaaaaaaaa aaaaaaaaa 1550

aaaaaaaaa aaaaaaaaa 1570
```

280

<210> 292
<211> 388
<212> PRT
<213> Homo sapiens

<400> 292
Met Lys Thr Leu Ile Ala Ala Tyr Ser Gly Val Leu Arg Gly Glu
 1   5   10   15

Arg Gln Ala Glu Ala Asp Arg Ser Gln Arg Ser His Gly Gly Pro
                20   25   30

Ala Leu Ser Arg Glu Gly Ser Gly Arg Trp Gly Thr Gly Ser Ser
                35   40   45

Ile Leu Ser Ala Leu Gln Asp Leu Phe Ser Val Thr Trp Leu Asn
                50   55   60

Arg Ser Lys Val Glu Lys Gln Leu Gln Val Ile Ser Val Leu Gln
                65   70   75

Trp Val Leu Ser Phe Leu Val Leu Gly Val Ala Cys Ser Ala Ile
                80   85   90

Leu Met Tyr Ile Phe Cys Thr Asp Cys Trp Leu Ile Ala Val Leu
                95   100   105

Tyr Phe Thr Trp Leu Val Phe Asp Trp Asn Thr Pro Lys Lys Gly
                110   115   120

Gly Arg Arg Ser Gln Trp Val Arg Asn Trp Ala Val Trp Arg Tyr
                125   130   135

Phe Arg Asp Tyr Phe Pro Ile Gln Leu Val Lys Thr His Asn Leu
                140   145   150

Leu Thr Thr Arg Asn Tyr Ile Phe Gly Tyr His Pro His Gly Ile
                155   160   165

Met Gly Leu Gly Ala Phe Cys Asn Phe Ser Thr Glu Ala Thr Glu
                170   175   180

Val Ser Lys Lys Phe Pro Gly Ile Arg Pro Tyr Leu Ala Thr Leu
                185   190   195

Ala Gly Asn Phe Arg Met Pro Val Leu Arg Glu Tyr Leu Met Ser
                200   205   210

Gly Gly Ile Cys Pro Val Ser Arg Asp Thr Ile Asp Tyr Leu Leu
                215   220   225

Ser Lys Asn Gly Ser Gly Asn Ala Ile Ile Ile Val Val Gly Gly
                230   235   240

Ala Ala Glu Ser Leu Ser Ser Met Pro Gly Lys Asn Ala Val Thr
                245   250   255

Leu Arg Asn Arg Lys Gly Phe Val Lys Leu Ala Leu Arg His Gly

281

Ala Asp Leu Val Pro Ile Tyr Ser Phe Gly Glu Asn Glu Val Tyr
                275   280   285

Lys Gln Val Ile Phe Glu Glu Gly Ser Trp Gly Arg Trp Val Gln
                290   295   300

Lys Lys Phe Gln Lys Tyr Ile Gly Phe Ala Pro Cys Ile Phe His
                305   310   315

Gly Arg Gly Leu Phe Ser Ser Asp Thr Trp Gly Leu Val Pro Tyr
                320   325   330

Ser Lys Pro Ile Thr Thr Val Val Gly Glu Pro Ile Thr Ile Pro
                335   340   345

Lys Leu Glu His Pro Thr Gln Gln Asp Ile Asp Leu Tyr His Thr
                350   355   360

Met Tyr Met Glu Ala Leu Val Lys Leu Phe Asp Lys His Lys Thr
                365   370   375

Lys Phe Gly Leu Pro Glu Thr Glu Val Leu Glu Val Asn
                380   385

<210> 293
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 293
 gctgacctgg ttcccatcta ctcc 24

<210> 294
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 294
 cccacagaca cccatgacac ttcc 24

<210> 295
<211> 50
<212> DNA
<213> Artificial

<220>

<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 295
aagaatgaat tgtacaaagc aggtgatctt cgaggagggc tcctggggcc 50

<210> 296
<211> 3060
<212> DNA
<213> Homo sapiens

<400> 296
gggcggcggg atggggggccg ggggcggcgg gcgccgcact cgctgaggcc 50

ccgacgcagg gccgggccgg gcccagggcc gaggagcgcg gcggccagag 100

cggggccgcg gaggcgacgc cggggacgcc cgcgcgacga gcaggtggcg 150

gcggctgcag gcttgtccag ccggaagccc tgagggcagc tgttcccact 200

ggctctgctg accttgtgcc ttggacggct gtcctcagcg aggggccgtg 250

cacccgctcc tgagcagcgc catgggcctg ctggccttcc tgaagaccca 300

gttcgtgctg cacctgctgg tcggctttgt cttcgtggtg agtggtctgg 350

tcatcaactt cgtccagctg tgcacgctgg cgctctggcc ggtcagcaag 400

cagctctacc gccgcctcaa ctgccgcctc gcctactcac tctggagcca 450

actggtcatg ctgctggagt ggtggtcctg cacggagtgt acactgttca 500

cggaccaggc cacggtagag cgctttggga aggagcacgc agtcatcatc 550

ctcaaccaca acttcgagat cgacttcctc tgtgggtgga ccatgtgtga 600

gcgcttcgga gtgctgggga gctccaaggt cctcgctaag aaggagctgc 650

tctacgtgcc cctcatcggc tggacgtggt actttctgga gattgtgttc 700

tgcaagcgga agtgggagga ggaccgggac accgtggtcg aagggctgag 750

gcgcctgtcg gactaccccg agtacatgtg gtttctcctg tactgcgagg 800

ggacgcgctt cacggagacc aagcaccgcg ttagcatgga ggtggcggct 850

gctaaggggc ttcctgtcct caagtaccac ctgctgccgc ggaccaaggg 900

cttcaccacc gcagtcaagt gcctccgggg gacagtcgca gctgtctatg 950

atgtaaccct gaacttcaga ggaaacaaga acccgtccct gctggggatc 1000

ctctacggga agaagtacga ggcggacatg tgcgtgagga gatttcctct 1050

ggaagacatc ccgctggatg aaaaggaagc agctcagtgg cttcataaac 1100

tgtaccagga gaaggacgcg ctccaggaga tatataatca gaagggcatg 1150

283

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tttccagggg agcagtttaa gcctgcccgg aggccgtgga ccctcctgaa 1200

cttcctgtcc tgggccacca ttctcctgtc tcccctcttc agttttgtct 1250

tgggcgtctt tgccagcgga tcacctctcc tgatcctgac tttcttgggg 1300

tttgtgggag cagcttcctt tggagttcgc agactgatag gagaatcgct 1350

tgaacctggg aggtggagat tgcagtgagc tgagatggca tcactgtact 1400

ccagcctagg caacagagca agactcagtc tcaaaaaaaa aaaaaaacaa 1450

aaaaacccca gaaattctgg agttgaactg tgtagttact gacatgaaaa 1500

attcactaga ggctgaacag cagatttgag caggcagaaa aaaatcagca 1550

agcttgaaga tggtaccttg agattttttca ggctaatgaa aaaagaatga 1600

aggaaaatta acagcctcag agacccatgg tgcaccgtca cacaaatcaa 1650

catatgcatg atgagagtcc cagaaggaga ggagagaaag ggtcagaaag 1700

aatggccaca agctgatgaa aaacagtaac ctacccactc aggaagctca 1750

gtgaactcca atgaggatga atatcagaga tccacaccta gatatttcat 1800

aatcaaagtg tcaaatgaca aagaatcttg aaagcagcaa gagatgagca 1850

acttatcttg ttcaaaggat ctttgatcag attaacagct catttctcct 1900

cagaaatcat gggagccagg agatagtggg atgaacactg ttgaaggcaa 1950

aaccttcaac tgtaattatt ggacttttga gtcttagatg gtcctgacct 2000

ctttgtcttc agggacagtt tttcaattta atccctaata acaattagtc 2050

aagcttcctt gacctgtagg aaggcctgtc tttaggccgg gcacagtggc 2100

ttacacctgt aatcccagca ctttgggagg cccagacggg tggatcattt 2150

ggggtcaggc tgatctcaaa ctcctgagtt caggtgatct gcccgcctca 2200

gcctcccaaa gtgttgtgat tgcaggcgtg agccactgcg cctggccgga 2250

atttctttt aaggctgaat gatgggggcc aggcacgatg gctcacgcct 2300

gtgatcccaa gtagcttgga ttgtaaacat gcaccaccat gcctggctaa 2350

tttttgtatt tttagtagag acgtgttagc caggctggtc tcgatctcct 2400

gacctcaagt gaccacctgc ctcagcctcc caaagtactg ggattacagg 2450

cgtgagccac tgtgcctggc cttgagcatc ttgtgatgtg cttattggcc 2500

atttgtatat cttctatctt ctttggggaa atgtctgttc aagtcctttg 2550

cctttttaaa ttttttattat ttatttattt atttattttg agacagggtc 2600
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284

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ttgttctgtt gcccaggctg gagtacagtg gcacagtctt ggctcactgc 2650

agcctcgacc tcctgggctg cagtgatcct cccacctcag cctcccttgt 2700

agctgtattt ttttgtattt tgtattttgt agctgtagtt tttgtatttt 2750

ttgtggagac agcatttcac catgatgccc aggctggtct tgaactcctg 2800

agctcaagtg atctgcctgc ttcagcctcc caaagtgctg ggattacaga 2850

catgagccac tgcacctggc aaactcccaa aattcaacac acacacacaa 2900

aaaaccacct gattcaaaat gggcagaggg gccgggtgtg gccccaacta 2950

ccagggagac tgaagtggga ggatcgcttg ggcatgagaa gtcgaggctg 3000

cagtgagtcg aggttgtgcg actgcattcc agcctggaca acagagtgag 3050

accctgtctc 3060
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<210> 297
<211> 368
<212> PRT
<213> Homo sapiens

<400> 297

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Met Gly Leu Leu Ala Phe Leu Lys Thr Gln Phe Val Leu His Leu
 1               5                  10                  15

Leu Val Gly Phe Val Phe Val Val Ser Gly Leu Val Ile Asn Phe
                20                  25                  30

Val Gln Leu Cys Thr Leu Ala Leu Trp Pro Val Ser Lys Gln Leu
                35                  40                  45

Tyr Arg Arg Leu Asn Cys Arg Leu Ala Tyr Ser Leu Trp Ser Gln
                50                  55                  60

Leu Val Met Leu Leu Glu Trp Trp Ser Cys Thr Glu Cys Thr Leu
                65                  70                  75

Phe Thr Asp Gln Ala Thr Val Glu Arg Phe Gly Lys Glu His Ala
                80                  85                  90

Val Ile Ile Leu Asn His Asn Phe Glu Ile Asp Phe Leu Cys Gly
                95                  100                 105

Trp Thr Met Cys Glu Arg Phe Gly Val Leu Gly Ser Ser Lys Val
                110                 115                 120

Leu Ala Lys Lys Glu Leu Leu Tyr Val Pro Leu Ile Gly Trp Thr
                125                 130                 135

Trp Tyr Phe Leu Glu Ile Val Phe Cys Lys Arg Lys Trp Glu Glu
                140                 145                 150

Asp Arg Asp Thr Val Val Glu Gly Leu Arg Arg Leu Ser Asp Tyr
                155                 160                 165
```

```
Pro Glu Tyr Met Trp Phe Leu Leu Tyr Cys Glu Gly Thr Arg Phe
             170                 175                 180

Thr Glu Thr Lys His Arg Val Ser Met Glu Val Ala Ala Ala Lys
             185                 190                 195

Gly Leu Pro Val Leu Lys Tyr His Leu Leu Pro Arg Thr Lys Gly
             200                 205                 210

Phe Thr Thr Ala Val Lys Cys Leu Arg Gly Thr Val Ala Ala Val
             215                 220                 225

Tyr Asp Val Thr Leu Asn Phe Arg Gly Asn Lys Asn Pro Ser Leu
             230                 235                 240

Leu Gly Ile Leu Tyr Gly Lys Lys Tyr Glu Ala Asp Met Cys Val
             245                 250                 255

Arg Arg Phe Pro Leu Glu Asp Ile Pro Leu Asp Glu Lys Glu Ala
             260                 265                 270

Ala Gln Trp Leu His Lys Leu Tyr Gln Glu Lys Asp Ala Leu Gln
             275                 280                 285

Glu Ile Tyr Asn Gln Lys Gly Met Phe Pro Gly Glu Gln Phe Lys
             290                 295                 300

Pro Ala Arg Arg Pro Trp Thr Leu Leu Asn Phe Leu Ser Trp Ala
             305                 310                 315

Thr Ile Leu Leu Ser Pro Leu Phe Ser Phe Val Leu Gly Val Phe
             320                 325                 330

Ala Ser Gly Ser Pro Leu Leu Ile Leu Thr Phe Leu Gly Phe Val
             335                 340                 345

Gly Ala Ala Ser Phe Gly Val Arg Arg Leu Ile Gly Glu Ser Leu
             350                 355                 360

Glu Pro Gly Arg Trp Arg Leu Gln
             365


<210> 298
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 298
  cttcctctgt gggtggacca tgtg 24

<210> 299
<211> 21
<212> DNA
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<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-21
<223> Synthetic construct.

<400> 299
 gccacctcca tgctaacgcg g 21

<210> 300
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 300
 ccaaggtcct cgctaagaag gagctgctct acgtgcccct catcg 45

<210> 301
<211> 1334
<212> DNA
<213> Homo sapiens

<400> 301
 gatattcttt attttttaaga atctgaagta ctatgcatca ctccctccaa 50

 tgtcctgggg cagccaccag gcatattcat ctttgtgtgt gttttctttt 100

 tgctttagca ctgggcact tcttgcttat ttctttggta ggaaaggggc 150

 tcagtttgtc ttgtggggtt ggtggcaggc aggccggctt acgcctgata 200

 cggccctggg ttagaaggga agggaagata aacttttata caaatgggga 250

 tagctggggt ctgagacctg cttcctcagt aaaattcctg ggatctgcct 300

 ataccttctt ttctctaacc tggcataccc tgcttaaagc ctctcagggc 350

 ttctctctgt tcttaggatc aaagtattta gagctacaag agccctcatg 400

 gtctggcccc tgcccccctg gccagcttca ttgtacatgt ggtgttctct 450

 tgtcgttcct gtaatgtggt atgccatggg gtctttgcac aagcctttcc 500

 tctttggctg gacactgttc cctgcccccc ccatactctt cctacttaat 550

 atgtagtcat cctgcagatt tcaattctaa catcattttc tccagggatc 600

 ctggcctgac agaatctcat cttgtttaat gctctcataa gaccacttgt 650

 ttccttttg cagcacttgc cactcagttg tatctttatg tgcgtttgtg 700

 gttgtatggg ttgtgtctgt tccccagaat gcccagctct gagctgcgtg 750

287

```
aggggtcaagg gcattgctgt gcctgccagg tatagtgcct acatgtggtg 800

ggtgctcatg ttttagagac taaatggagg aggagatgag gaaaagattg 850

aaatctctca gttcaccaga tggtgtaggg cccagcattg taaattcaca 900

cgttgactgt gcttgtgaat tatctgggga tgcaggtcct gattcagtag 950

gcccaggttg ggcatctcta acaaactccc acgtgatgct gatgctggtc 1000

ctatgaacta tactaaatag taagaatcta tggagccagg ctgggcatgg 1050

tggctcacac ctatgatccc agcactttgg gaggctgagg caggctgatc 1100

acctggagtc aggatttcaa gactagcctg gccaacatgg tggaacccca 1150

tctgtactaa aaatacacaa attagctggg catggtggca catgcctgta 1200

gtcccagcta cttgggaggc tgaagcaaga gaatcgcttg aacctgggag 1250

gcggaggttg cagtgagccg agatcaggcc actgtattcc aaccagggtg 1300

acagagtgag actctatgtc caaaaaaaaa aaaa 1334
```

<210> 302
<211> 143
<212> PRT
<213> Homo sapiens

<400> 302

```
Met His His Ser Leu Gln Cys Pro Gly Ala Ala Thr Arg His Ile
 1               5                  10                  15

His Leu Cys Val Cys Phe Ser Phe Ala Leu Ala Leu Gly His Phe
                20                  25                  30

Leu Leu Ile Ser Leu Val Gly Lys Gly Leu Ser Leu Ser Cys Gly
                35                  40                  45

Val Gly Gly Arg Gln Ala Gly Leu Arg Leu Ile Arg Pro Trp Val
                50                  55                  60

Arg Arg Glu Gly Lys Ile Asn Phe Tyr Thr Asn Gly Asp Ser Trp
                65                  70                  75

Gly Leu Arg Pro Ala Ser Ser Val Lys Phe Leu Gly Ser Ala Tyr
                80                  85                  90

Thr Phe Phe Ser Leu Thr Trp His Thr Leu Leu Lys Ala Ser Gln
                95                  100                 105

Gly Phe Ser Leu Phe Leu Gly Ser Lys Tyr Leu Glu Leu Gln Glu
                110                 115                 120

Pro Ser Trp Ser Gly Pro Cys Pro Pro Gly Gln Leu His Cys Thr
                125                 130                 135

Cys Gly Val Leu Leu Ser Phe Leu
```

288

<210> 303
<211> 1768
<212> DNA
<213> Homo sapiens

<400> 303
ggctggactg gaactcctgg tcccaagtga tccacccgcc tcagcctccc 50

aaggtgctgt gattataggt gtaagccacc gtgtctggcc tctgaacaac 100

tttttcagca actaaaaaag ccacaggagt tgaactgcta ggattctgac 150

tatgctgtgg tggctagtgc tcctactcct acctacatta aaatctgttt 200

tttgttctct tgtaactagc ctttaccttc ctaacacaga ggatctgtca 250

ctgtggctct ggcccaaacc tgaccttcac tctggaacga gaacagaggt 300

ttctacccac accgtcccct cgaagccggg gacagcctca ccttgctggc 350

ctctcgctgg agcagtgccc tcaccaactg tctcacgtct ggaggcactg 400

actcgggcag tgcaggtagc tgagcctctt ggtagctgcg gctttcaagg 450

tgggccttgc cctggccgta gaagggattg acaagcccga agatttcata 500

ggcgatggct cccactgccc aggcatcagc cttgctgtag tcaatcactg 550

ccctggggcc aggacgggcc gtggacacct gctcagaagc agtgggtgag 600

acatcacgct gcccgcccat ctaacctttt catgtcctgc acatcacctg 650

atccatgggc taatctgaac tctgtcccaa ggaacccaga gcttgagtga 700

gctgtggctc agacccagaa ggggtctgct tagaccacct ggtttatgtg 750

acaggacttg cattctcctg gaacatgagg gaacgccgga ggaaagcaaa 800

gtggcaggga aggaacttgt gccaaattat gggtcagaaa agatggaggt 850

gttgggttat cacaaggcat cgagtctcct gcattcagtg gacatgtggg 900

ggaagggctg ccgatggcgc atgacacact cgggactcac ctctggggcc 950

atcagacagc cgtttccgcc ccgatccacg taccagctgc tgaagggcaa 1000

ctgcaggccg atgctctcat cagccaggca gcagccaaaa tctgcgatca 1050

ccagccaggg gcagccgtct gggaaggagc aagcaaagtg accatttctc 1100

ctcccctcct tccctctgag aggccctcct atgtccctac taaagccacc 1150

agcaagacat agctgacagg ggctaatggc tcagtgttgg cccaggaggt 1200

cagcaaggcc tgagagctga tcagaagggc ctgctgtgcg aacacggaaa 1250

tgcctccagt aagcacaggc tgcaaaatcc ccaggcaaag gactgtgtgg 1300

ctcaatttaa atcatgttct agtaattgga gctgtcccca agaccaaagg 1350

agctagagct tggttcaaat gatctccaag ggcccttata ccccaggaga 1400

ctttgatttg aatttgaaac cccaaatcca aacctaagaa ccaggtgcat 1450

taagaatcag ttattgccgg gtgtggtggc ctgtaatgcc aacattttgg 1500

gaggccgagg cgggtagatc acctgaggtc aggagttcaa gaccagcctg 1550

gccaacatgg tgaaacccct gtctctacta aaaatacaaa aaaactagcc 1600

aggcatggtg gtgtgtgcct gtatcccagc tactcgggag gctgagacag 1650

gagaattact tgaacctggg aggtgaagga ggctgagaca ggagaatcac 1700

ttcagcctga gcaacacagc gagactctgt ctcagaaaaa ataaaaaaag 1750

aattatggtt atttgtaa 1768

<210> 304
<211> 109
<212> PRT
<213> Homo sapiens

<400> 304
    Met Leu Trp Trp Leu Val Leu Leu Leu Pro Thr Leu Lys Ser
    1   5   10   15

    Val Phe Cys Ser Leu Val Thr Ser Leu Tyr Leu Pro Asn Thr Glu
                    20   25   30

    Asp Leu Ser Leu Trp Leu Trp Pro Lys Pro Asp Leu His Ser Gly
                    35   40   45

    Thr Arg Thr Glu Val Ser Thr His Thr Val Pro Ser Lys Pro Gly
                    50   55   60

    Thr Ala Ser Pro Cys Trp Pro Leu Ala Gly Ala Val Pro Ser Pro
                    65   70   75

    Thr Val Ser Arg Leu Glu Ala Leu Thr Arg Ala Val Gln Val Ala
                    80   85   90

    Glu Pro Leu Gly Ser Cys Gly Phe Gln Gly Gly Pro Cys Pro Gly
                    95   100   105

Arg Arg Arg Asp

<210> 305
<211> 989
<212> DNA
<213> Homo sapiens

<400> 305

290

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gcgggcccgc gagtccgaga cctgtcccag gagctccagc tcacgtgacc 50

tgtcactgcc tcccgccgcc tcctgcccgc gccatgaccc agccggtgcc 100

ccggctctcc gtgcccgccg cgctggccct gggctcagcc gcactgggcg 150

ccgccttcgc cactggcctc ttcctgggga ggcggtgccc cccatggcga 200

ggccggcgag agcagtgcct gcttccccccc gaggacagcc gcctgtggca 250

gtatcttctg agccgctcca tgcgggagca cccggcgctg cgaagcctga 300

ggctgctgac cctggagcag ccgcaggggg attctatgat gacctgcgag 350

caggcccagc tcttggccaa cctggcgcgg ctcatccagg ccaagaaggc 400

gctggacctg ggcaccttca cgggctactc cgccctggcc ctggccctgg 450

cgctgcccgc ggacgggcgc gtggtgacct gcgaggtgga cgcgcagccc 500

ccggagctgg acggcccct gtggaggcag gccgaggcgg agcacaagat 550

cgacctccgg ctgaagcccg ccttggagac cctggacgag ctgctggcgg 600

cgggcgaggc cggcaccttc gacgtggccg tggtggatgc ggacaaggag 650

aactgctccg cctactacga gcgctgcctg cagctgctgc gacccggagg 700

catcctcgcc gtcctcagag tcctgtggcg cgggaaggtg ctgcaacctc 750

cgaaagggga cgtggcggcc gagtgtgtgc gaaacctaaa cgaacgcatc 800

cggcgggacg tcagggtcta catcagcctc ctgcccctgg gcgatggact 850

caccttggcc ttcaagatct agggctggcc cctagtgagt gggctcgagg 900

gagggttgcc tgggaacccc aggaattgac cctgagtttt aaattcgaaa 950

ataaagtggg gctgggacac aaaaaaaaaa aaaaaaaaa 989
```

<210> 306
<211> 262
<212> PRT
<213> Homo sapiens

<400> 306
```
Met Thr Gln Pro Val Pro Arg Leu Ser Val Pro Ala Ala Leu Ala
 1               5                  10                  15

Leu Gly Ser Ala Ala Leu Gly Ala Ala Phe Ala Thr Gly Leu Phe
                20                  25                  30

Leu Gly Arg Arg Cys Pro Pro Trp Arg Gly Arg Arg Glu Gln Cys
                35                  40                  45

Leu Leu Pro Pro Glu Asp Ser Arg Leu Trp Gln Tyr Leu Leu Ser
                50                  55                  60
```

291

```
Arg Ser Met Arg Glu His Pro Ala Leu Arg Ser Leu Arg Leu Leu
            65                  70                      75

Thr Leu Glu Gln Pro Gln Gly Asp Ser Met Met Thr Cys Glu Gln
            80                  85                      90

Ala Gln Leu Leu Ala Asn Leu Ala Arg Leu Ile Gln Ala Lys Lys
            95                  100                     105

Ala Leu Asp Leu Gly Thr Phe Thr Gly Tyr Ser Ala Leu Ala Leu
            110                 115                     120

Ala Leu Ala Leu Pro Ala Asp Gly Arg Val Val Thr Cys Glu Val
            125                 130                     135

Asp Ala Gln Pro Pro Glu Leu Gly Arg Pro Leu Trp Arg Gln Ala
            140                 145                     150

Glu Ala Glu His Lys Ile Asp Leu Arg Leu Lys Pro Ala Leu Glu
            155                 160                     165

Thr Leu Asp Glu Leu Leu Ala Ala Gly Glu Ala Gly Thr Phe Asp
            170                 175                     180

Val Ala Val Val Asp Ala Asp Lys Glu Asn Cys Ser Ala Tyr Tyr
            185                 190                     195

Glu Arg Cys Leu Gln Leu Leu Arg Pro Gly Gly Ile Leu Ala Val
            200                 205                     210

Leu Arg Val Leu Trp Arg Gly Lys Val Leu Gln Pro Pro Lys Gly
            215                 220                     225

Asp Val Ala Ala Glu Cys Val Arg Asn Leu Asn Glu Arg Ile Arg
            230                 235                     240

Arg Asp Val Arg Val Tyr Ile Ser Leu Leu Pro Leu Gly Asp Gly
            245                 250                     255

Leu Thr Leu Ala Phe Lys Ile
            260
```

<210> 307
<211> 2272
<212> DNA
<213> Homo sapiens

<400> 307
```
ccgccgccgc agccgctacc gccgctgcag ccgctttccg cggcctgggc 50

ctctcgccgt cagcatgcca cacgccttca gcccggggga cttggtgttc 100

gctaagatga agggctaccc tcactggcct gccaggatcg acgacatcgc 150

ggatggcgcc gtgaagcccc cacccaacaa gtaccccatc tttttctttg 200

gcacacacga aacagccttc ctgggaccca aggacctgtt cccctacgac 250
```

```
aaatgtaaag acaagtacgg gaagcccaac aagaggaaag gcttcaatga  300

agggctgtgg gagatccaga acaacccccca cgccagctac agcgcccctc  350

cgccagtgag ctcctccgac agcgaggccc ccgaggccaa ccccgccgac  400

ggcagtgacg ctgacgagga cgatgaggac cggggggtca tggccgtcac  450

agcggtaacc gccacagctg ccagcgacag gatggagagc gactcagact  500

cagacaagag tagcgacaac agtggcctga agaggaagac gcctgcgcta  550

aagatgtcgg tctcgaaacg agcccgaaag gcctccagcg acctggatca  600

ggccagcgtg tccccatccg aagaggagaa ctcggaaagc tcatctgagt  650

cggagaagac cagcgaccag gacttcacac ctgagaagaa agcagcggtc  700

cgggcgccac ggagggggccc tctggggggga cggaaaaaaa agaaggcgcc  750

gtcagcctcc gactccgact ccaaggccga ttcggacggg gccaagcctg  800

agccggtggc catggcgcgg tcggcgtcct cctcctcctc ttcctcctcc  850

tcctccgact ccgatgtgtc tgtgaagaag cctccgaggg gcaggaagcc  900

agcggagaag cctctcccga agccgcgagg gcggaaaccg aagcctgaac  950

ggcctccgtc cagctccagc agtgacagtg acagcgacga ggtggaccgc 1000

atcagtgagt ggaagcggcg ggacgaggcg cggaggcgcg agctggaggc 1050

ccggcggcgg cgagagcagg aggaggagct gcggcgcctg cgggagcagg 1100

agaaggagga gaaggagcgg aggcgcgagc gggccgaccg cgggggaggct 1150

gagcggggca gcggcggcag cagcggggac gagctcaggg aggacgatga 1200

gcccgtcaag aagcggggac gcaagggccg gggccggggt ccccccgtcct 1250

cctctgactc cgagcccgag gccgagctgg agagagaggc caagaaatca 1300

gcgaagaagc cgcagtcctc aagcacagag cccgccagga aacctggcca 1350

gaaggagaag agagtgcggc ccgaggagaa gcaacaagcc aagcccgtga 1400

aggtggagcg gacccggaag cggtccgagg gcttctcgat ggacaggaag 1450

gtagagaaga agaaagagcc ctccgtggag gagaagctgc agaagctgca 1500

cagtgagatc aagtttgccc taaaggtcga cagcccggac gtgaagaggt 1550

gcctgaatgc cctagaggag ctgggaaccc tgcaggtgac ctctcagatc 1600

ctccagaaga acacagacgt ggtggccacc ttgaagaaga ttcgccgtta 1650

caaagcgaac aaggacgtaa tggagaaggc agcagaagtc tatacccggc 1700
```

293

```
tcaagtcgcg ggtcctcggc ccaaagatcg aggcggtgca gaaagtgaac 1750

aaggctggga tggagaagga gaaggccgag gagaagctgg ccggggagga 1800

gctggccggg gaggaggccc cccaggagaa ggcggaggac aagcccagca 1850

ccgatctctc agccccagtg aatggcgagg ccacatcaca gaaggggggag 1900

agcgcagagg acaaggagca cgaggagggt cgggactcgg aggagggggcc 1950

aaggtgtggc tcctctgaag acctgcacga cagcgtacgg gagggtcccg 2000

acctggacag gcctgggagc gaccggcagg agcgcgagag ggcacggggg 2050

gactcggagg ccctggacga ggagagctga gccgcgggca gccaggccca 2100

gcccccgccc gagctcaggc tgcccctctc cttccccggc tcgcaggaga 2150

gcagagcaga gaactgtggg gaacgctgtg ctgtttgtat ttgttccctt 2200

gggttttttt ttcctgccta atttctgtga tttccaacca acatgaaatg 2250

actataaacg gttttttaat ga 2272
```

<210> 308
<211> 671
<212> PRT
<213> Homo sapiens

<400> 308

```
Met Pro His Ala Phe Lys Pro Gly Asp Leu Val Phe Ala Lys Met
 1               5                  10                  15

Lys Gly Tyr Pro His Trp Pro Ala Arg Ile Asp Asp Ile Ala Asp
             20                  25                  30

Gly Ala Val Lys Pro Pro Asn Lys Tyr Pro Ile Phe Phe Phe
             35                  40                  45

Gly Thr His Glu Thr Ala Phe Leu Gly Pro Lys Asp Leu Phe Pro
             50                  55                  60

Tyr Asp Lys Cys Lys Asp Lys Tyr Gly Lys Pro Asn Lys Arg Lys
             65                  70                  75

Gly Phe Asn Glu Gly Leu Trp Glu Ile Gln Asn Asn Pro His Ala
             80                  85                  90

Ser Tyr Ser Ala Pro Pro Pro Val Ser Ser Asp Ser Glu Ala
             95                  100                 105

Pro Glu Ala Asn Pro Ala Asp Gly Ser Asp Ala Asp Glu Asp Asp
             110                 115                 120

Glu Asp Arg Gly Val Met Ala Val Thr Ala Val Thr Ala Thr Ala
             125                 130                 135

Ala Ser Asp Arg Met Glu Ser Asp Ser Asp Ser Asp Lys Ser Ser
```

294
```

                    140                    145                    150

Asp Asn Ser Gly Leu Lys Arg Lys Thr Pro Ala Leu Lys Met Ser
                155                    160                    165

Val Ser Lys Arg Ala Arg Lys Ala Ser Ser Asp Leu Asp Gln Ala
                170                    175                    180

Ser Val Ser Pro Ser Glu Glu Glu Asn Ser Glu Ser Ser Ser Glu
                185                    190                    195

Ser Glu Lys Thr Ser Asp Gln Asp Phe Thr Pro Glu Lys Lys Ala
                200                    205                    210

Ala Val Arg Ala Pro Arg Arg Gly Pro Leu Gly Gly Arg Lys Lys
                215                    220                    225

Lys Lys Ala Pro Ser Ala Ser Asp Ser Asp Ser Lys Ala Asp Ser
                230                    235                    240

Asp Gly Ala Lys Pro Glu Pro Val Ala Met Ala Arg Ser Ala Ser
                245                    250                    255

Ser Ser Ser Ser Ser Ser Ser Ser Ser Asp Ser Asp Val Ser Val
                260                    265                    270

Lys Lys Pro Pro Arg Gly Arg Lys Pro Ala Glu Lys Pro Leu Pro
                275                    280                    285

Lys Pro Arg Gly Arg Lys Pro Lys Pro Glu Arg Pro Pro Ser Ser
                290                    295                    300

Ser Ser Ser Asp Ser Asp Ser Asp Glu Val Asp Arg Ile Ser Glu
                305                    310                    315

Trp Lys Arg Arg Asp Glu Ala Arg Arg Arg Glu Leu Glu Ala Arg
                320                    325                    330

Arg Arg Arg Glu Gln Glu Glu Glu Leu Arg Arg Leu Arg Glu Gln
                335                    340                    345

Glu Lys Glu Glu Lys Glu Arg Arg Arg Glu Arg Ala Asp Arg Gly
                350                    355                    360

Glu Ala Glu Arg Gly Ser Gly Gly Ser Ser Gly Asp Glu Leu Arg
                365                    370                    375

Glu Asp Asp Glu Pro Val Lys Lys Arg Gly Arg Lys Gly Arg Gly
                380                    385                    390

Arg Gly Pro Pro Ser Ser Ser Asp Ser Glu Pro Glu Ala Glu Leu
                395                    400                    405

Glu Arg Glu Ala Lys Lys Ser Ala Lys Lys Pro Gln Ser Ser Ser
                410                    415                    420

Thr Glu Pro Ala Arg Lys Pro Gly Gln Lys Glu Lys Arg Val Arg
                425                    430                    435

295

```
Pro Glu Glu Lys Gln Gln Ala Lys Pro Val Lys Val Glu Arg Thr
              440                 445                 450

Arg Lys Arg Ser Glu Gly Phe Ser Met Asp Arg Lys Val Glu Lys
              455                 460                 465

Lys Lys Glu Pro Ser Val Glu Glu Lys Leu Gln Lys Leu His Ser
              470                 475                 480

Glu Ile Lys Phe Ala Leu Lys Val Asp Ser Pro Asp Val Lys Arg
              485                 490                 495

Cys Leu Asn Ala Leu Glu Glu Leu Gly Thr Leu Gln Val Thr Ser
              500                 505                 510

Gln Ile Leu Gln Lys Asn Thr Asp Val Val Ala Thr Leu Lys Lys
              515                 520                 525

Ile Arg Arg Tyr Lys Ala Asn Lys Asp Val Met Glu Lys Ala Ala
              530                 535                 540

Glu Val Tyr Thr Arg Leu Lys Ser Arg Val Leu Gly Pro Lys Ile
              545                 550                 555

Glu Ala Val Gln Lys Val Asn Lys Ala Gly Met Glu Lys Glu Lys
              560                 565                 570

Ala Glu Glu Lys Leu Ala Gly Glu Glu Leu Ala Gly Glu Glu Ala
              575                 580                 585

Pro Gln Glu Lys Ala Glu Asp Lys Pro Ser Thr Asp Leu Ser Ala
              590                 595                 600

Pro Val Asn Gly Glu Ala Thr Ser Gln Lys Gly Glu Ser Ala Glu
              605                 610                 615

Asp Lys Glu His Glu Glu Gly Arg Asp Ser Glu Glu Gly Pro Arg
              620                 625                 630

Cys Gly Ser Ser Glu Asp Leu His Asp Ser Val Arg Glu Gly Pro
              635                 640                 645

Asp Leu Asp Arg Pro Gly Ser Asp Arg Gln Glu Arg Glu Arg Ala
              650                 655                 660

Arg Gly Asp Ser Glu Ala Leu Asp Glu Glu Ser
              665                 670
```

<210> 309
<211> 3871
<212> DNA
<213> Homo sapiens

<400> 309
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 gttggttctc ctggatcttc accttaccaa ctgcagatct tgggactcat 50

 cagcctcaat aattatatta aattaacacc atttgaaaga gaacattgtt 100
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ttcatcatga atgctaataa agatgaaaga cttaaagcca gaagccaaga 150

tttttcacctt tttcctgctt tgatgatgct aagcatgacc atgttgtttc 200

ttccagtcac tggcactttg aagcaaaata ttccaagact caagctaacc 250

tacaaagact tgctgctttc aaatagctgt attcccttt tgggttcatc 300

agaaggactg gattttcaaa ctcttctctt agatgaggaa agaggcaggc 350

tgctcttggg agccaaagac cacatctttc tactcagtct ggttgactta 400

aacaaaaatt ttaagaagat ttattggcct gctgcaaagg aacgggtgga 450

attatgtaaa ttagctggga aagatgccaa tacagaatgt gcaaatttca 500

tcagagtact tcagccctat aacaaaactc acatatatgt gtgtggaact 550

ggagcatttc atccaatatg tgggtatatt gatcttggag tctacaagga 600

ggatattata ttcaaactag acacacataa tttggagtct ggcagactga 650

aatgtccttt cgatcctcag cagccttttg cttcagtaat gacagatgag 700

tacctctact ctggaacagc ttctgatttc cttggcaaag atactgcatt 750

cactcgatcc cttgggccta ctcatgacca ccactacatc agaactgaca 800

tttcagagca ctactggctc aatggagcaa aatttattgg aactttcttc 850

ataccagaca cctacaatcc agatgatgat aaaatatatt tcttctttcg 900

tgaatcatct caagaaggca gtacctccga taaaaccatc ctttctcgag 950

ttggaagagt ttgtaagaat gatgtaggag gacaacgcag cctgataaac 1000

aagtggacga cttttcttaa ggccagactg atttgctcaa ttcctggaag 1050

tgatggggca gatacttact ttgatgagct tcaagatatt tatttactcc 1100

ccacaagaga tgaaagaaat cctgtagtat atggagtctt tactacaacc 1150

agctccatct tcaaaggctc tgctgtttgt gtgtatagca tggctgacat 1200

cagagcagtt tttaatggtc catatgctca taaggaaagt gcagaccatc 1250

gttgggtgca gtatgatggg agaattcctt atccacggcc tggtacatgt 1300

ccaagcaaaa cctatgaccc actgattaag tccacccgag attttccaga 1350

tgatgtcatc agtttcataa agcggcactc tgtgatgtat aagtccgtat 1400

acccagttgc aggaggacca acgttcaaga gaatcaatgt ggattacaga 1450

ctgacacaga tagtggtgga tcatgtcatt gcagaagatg gccagtacga 1500

tgtaatgttt cttggaacag acattggaac tgtcctcaaa gttgtcagca 1550

297

```
tttcaaagga aaagtggaat atggaagagg tagtgctgga ggagttgcag 1600

atattcaagc actcatcaat catcttgaac atggaattgt ctctgaagca 1650

gcaacaattg tacattggtt cccgagatgg attagttcag ctctccttgc 1700

acagatgcga cacttatggg aaagcttgcg cagactgttg tcttgccaga 1750

gaccccctact gtgcctggga tggaaatgca tgctctcgat atgctcctac 1800

ttctaaaagg agagctagac gccaagatgt aaaatatggc gacccaatca 1850

cccagtgctg ggacatcgaa gacagcatta gtcatgaaac tgctgatgaa 1900

aaggtgattt ttggcattga atttaactca acctttctgg aatgtatacc 1950

taaatcccaa caagcaacta ttaaatggta tatccagagg tcaggggatg 2000

agcatcgaga ggagttgaag cccgatgaaa gaatcatcaa aacggaatat 2050

gggctactga ttcgaagttt gcagaagaag gattctggga tgtattactg 2100

caaagcccag gagcacactt tcatccacac catagtgaag ctgactttga 2150

atgtcattga gaatgaacag atggaaaata cccagagggc agagcatgag 2200

gaggggcagg tcaaggatct attggctgag tcacggttga gatacaaaga 2250

ctacatccaa atccttagca gcccaaactt cagcctcgac cagtactgcg 2300

aacagatgtg gcacagggag aagcggagac agagaaacaa gggggggccca 2350

aagtggaagc acatgcagga aatgaagaag aaacgaaatc gaagacatca 2400

cagagacctg gatgagctcc ctagagctgt agccacgtag ttttctactt 2450

aatttaaaga aaagaattcc ttacctataa aaacattgcc ttctgttttg 2500

tatatccctt atagtaattc ataaatgctt cccatggagt tttgctaagg 2550

cacaagacaa taatctgaat aagacaatat gtgatgaata taagaaaggg 2600

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298

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<212> PRT
<213> Homo sapiens

<400> 310

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    Phe Leu Pro Val Thr Gly Thr Leu Lys Gln Asn Ile Pro Arg Leu
                    35                  40                  45

    Lys Leu Thr Tyr Lys Asp Leu Leu Leu Ser Asn Ser Cys Ile Pro
                    50                  55                  60

    Phe Leu Gly Ser Ser Glu Gly Leu Asp Phe Gln Thr Leu Leu Leu
                    65                  70                  75

    Asp Glu Glu Arg Gly Arg Leu Leu Leu Gly Ala Lys Asp His Ile
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                  80                    85                    90
Phe Leu Leu Ser Leu Val Asp Leu Asn Lys Asn Phe Lys Lys Ile
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Tyr Trp Pro Ala Ala Lys Glu Arg Val Glu Leu Cys Lys Leu Ala
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Gly Lys Asp Ala Asn Thr Glu Cys Ala Asn Phe Ile Arg Val Leu
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Gln Pro Tyr Asn Lys Thr His Ile Tyr Val Cys Gly Thr Gly Ala
                140                   145                   150

Phe His Pro Ile Cys Gly Tyr Ile Asp Leu Gly Val Tyr Lys Glu
                155                   160                   165

Asp Ile Ile Phe Lys Leu Asp Thr His Asn Leu Glu Ser Gly Arg
                170                   175                   180

Leu Lys Cys Pro Phe Asp Pro Gln Gln Pro Phe Ala Ser Val Met
                185                   190                   195

Thr Asp Glu Tyr Leu Tyr Ser Gly Thr Ala Ser Asp Phe Leu Gly
                200                   205                   210

Lys Asp Thr Ala Phe Thr Arg Ser Leu Gly Pro Thr His Asp His
                215                   220                   225

His Tyr Ile Arg Thr Asp Ile Ser Glu His Tyr Trp Leu Asn Gly
                230                   235                   240

Ala Lys Phe Ile Gly Thr Phe Phe Ile Pro Asp Thr Tyr Asn Pro
                245                   250                   255

Asp Asp Asp Lys Ile Tyr Phe Phe Phe Arg Glu Ser Ser Gln Glu
                260                   265                   270

Gly Ser Thr Ser Asp Lys Thr Ile Leu Ser Arg Val Gly Arg Val
                275                   280                   285

Cys Lys Asn Asp Val Gly Gly Gln Arg Ser Leu Ile Asn Lys Trp
                290                   295                   300

Thr Thr Phe Leu Lys Ala Arg Leu Ile Cys Ser Ile Pro Gly Ser
                305                   310                   315

Asp Gly Ala Asp Thr Tyr Phe Asp Glu Leu Gln Asp Ile Tyr Leu
                320                   325                   330

Leu Pro Thr Arg Asp Glu Arg Asn Pro Val Val Tyr Gly Val Phe
                335                   340                   345

Thr Thr Thr Ser Ser Ile Phe Lys Gly Ser Ala Val Cys Val Tyr
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Ser Met Ala Asp Ile Arg Ala Val Phe Asn Gly Pro Tyr Ala His
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300

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            395   400   405

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            410   415   420

Ile Lys Arg His Ser Val Met Tyr Lys Ser Val Tyr Pro Val Ala
            425   430   435

Gly Gly Pro Thr Phe Lys Arg Ile Asn Val Asp Tyr Arg Leu Thr
            440   445   450

Gln Ile Val Val Asp His Val Ile Ala Glu Asp Gly Gln Tyr Asp
            455   460   465

Val Met Phe Leu Gly Thr Asp Ile Gly Thr Val Leu Lys Val Val
            470   475   480

Ser Ile Ser Lys Glu Lys Trp Asn Met Glu Glu Val Val Leu Glu
            485   490   495

Glu Leu Gln Ile Phe Lys His Ser Ser Ile Ile Leu Asn Met Glu
            500   505   510

Leu Ser Leu Lys Gln Gln Gln Leu Tyr Ile Gly Ser Arg Asp Gly
            515   520   525

Leu Val Gln Leu Ser Leu His Arg Cys Asp Thr Tyr Gly Lys Ala
            530   535   540

Cys Ala Asp Cys Cys Leu Ala Arg Asp Pro Tyr Cys Ala Trp Asp
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Gly Asn Ala Cys Ser Arg Tyr Ala Pro Thr Ser Lys Arg Arg Ala
            560   565   570

Arg Arg Gln Asp Val Lys Tyr Gly Asp Pro Ile Thr Gln Cys Trp
            575   580   585

Asp Ile Glu Asp Ser Ile Ser His Glu Thr Ala Asp Glu Lys Val
            590   595   600

Ile Phe Gly Ile Glu Phe Asn Ser Thr Phe Leu Glu Cys Ile Pro
            605   610   615

Lys Ser Gln Gln Ala Thr Ile Lys Trp Tyr Ile Gln Arg Ser Gly
            620   625   630

Asp Glu His Arg Glu Glu Leu Lys Pro Asp Glu Arg Ile Ile Lys
            635   640   645

Thr Glu Tyr Gly Leu Leu Ile Arg Ser Leu Gln Lys Lys Asp Ser
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Gly Met Tyr Tyr Cys Lys Ala Gln Glu His Thr Phe Ile His Thr

301

Ile Val Lys Leu Thr Leu Asn Val Ile Glu Asn Glu Gln Met Glu
              680   685   690

Asn Thr Gln Arg Ala Glu His Glu Glu Gly Gln Val Lys Asp Leu
              695   700   705

Leu Ala Glu Ser Arg Leu Arg Tyr Lys Asp Tyr Ile Gln Ile Leu
              710   715   720

Ser Ser Pro Asn Phe Ser Leu Asp Gln Tyr Cys Glu Gln Met Trp
              725   730   735

His Arg Glu Lys Arg Arg Gln Arg Asn Lys Gly Gly Pro Lys Trp
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Lys His Met Gln Glu Met Lys Lys Lys Arg Asn Arg Arg His His
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Arg Asp Leu Asp Glu Leu Pro Arg Ala Val Ala Thr
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304

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<211> 370
<212> PRT
<213> Homo sapiens

<400> 315

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Gln Arg Leu Glu Gln Arg Arg Gln Gln Ala Ser Glu Arg Glu Ala
            35              40              45

Pro Ser Ile Glu Gln Arg Leu Gln Glu Val Arg Glu Ser Ile Arg
            50              55              60

Arg Ala Gln Val Ser Gln Val Lys Gly Ala Ala Arg Leu Ala Leu
            65              70              75

Leu Gln Gly Ala Gly Leu Asp Val Glu Arg Trp Leu Lys Pro Ala
            80              85              90

Met Thr Gln Ala Gln Asp Glu Val Glu Gln Glu Arg Arg Leu Ser
            95              100             105

Glu Ala Arg Leu Ser Gln Arg Asp Leu Ser Pro Thr Ala Glu Asp
            110             115             120

Ala Glu Leu Ser Asp Phe Glu Glu Cys Glu Glu Thr Gly Glu Leu
            125             130             135

Phe Glu Glu Pro Ala Pro Gln Ala Leu Ala Thr Arg Ala Leu Pro
            140             145             150

Cys Pro Ala His Val Val Phe Arg Tyr Gln Ala Gly Arg Glu Asp
            155             160             165

Glu Leu Thr Ile Thr Glu Gly Glu Trp Leu Glu Val Ile Glu Glu
            170             175             180

Gly Asp Ala Asp Glu Trp Val Lys Ala Arg Asn Gln His Gly Glu
            185             190             195

Val Gly Phe Val Pro Glu Arg Tyr Leu Asn Phe Pro Asp Leu Ser
            200             205             210

Leu Pro Glu Ser Ser Gln Asp Ser Asp Asn Pro Cys Gly Ala Glu
            215             220             225

Pro Thr Ala Phe Leu Ala Gln Ala Leu Tyr Ser Tyr Thr Gly Gln
            230             235             240

Ser Ala Glu Glu Leu Ser Phe Pro Glu Gly Ala Leu Ile Arg Leu
            245             250             255

Leu Pro Arg Ala Gln Asp Gly Val Asp Asp Gly Phe Trp Arg Gly
            260             265             270

Glu Phe Gly Gly Arg Val Gly Val Phe Pro Ser Leu Leu Val Glu
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Glu Leu Leu Gly Pro Pro Gly Pro Pro Glu Leu Ser Asp Pro Glu
            290             295             300

Gln Met Leu Pro Ser Pro Ser Pro Pro Ser Phe Ser Pro Pro Ala
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306

Pro Thr Ser Val Leu Asp Gly Pro Pro Ala Pro Val Leu Pro Gly
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Asp Lys Ala Leu Asp Phe Pro Gly Phe Leu Asp Met Met Ala Pro
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Arg Leu Arg Pro Met Arg Pro Pro Pro Pro Pro Ala Lys Ala
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Pro Asp Pro Gly His Pro Asp Pro Leu Thr
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ccagctaatt tttgttttgt tttgtttgga gacagagtct cgctattgtc 3750

accagggctg gaatgatttc agctcactgc aaccttcgcc acctgggttc 3800

cagcaattct cctgcctcag cctcccgagt agctgagatt ataggcacct 3850

309

```
accaccacgc ccggctaatt tttgtatttt tagtagagac ggggtttcac 3900

catgttggcc aggctggtct cgaactcctg accttaggtg atccactcgc 3950

cttcatctcc caaagtgctg ggattacagg cgtgagccac cgtgcctggc 4000

cacgcccaac taattttgt attttagta gagacagggt ttcaccatgt 4050

tggccaggct gctcttgaac tcctgacctc aggtaatcga cctgcctcgg 4100

cctcccaaag tgctgggatt acaggtgtga gccaccacgc ccggtacata 4150

ttttttaaat tgaattctac tatttatgtg atccttttgg agtcagacag 4200

atgtggttgc atcctaactc catgtctctg agcattagat ttctcatttg 4250

ccaataataa tacctccctt agaagtttgt tgtgaggatt aaataatgta 4300

aataaagaac tagcataaca ctcaaaaaaa aaaaaaaaaa aaaaaaaaaa 4350

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 4400

aaggaaa 4407
```

<210> 317
<211> 837
<212> PRT
<213> Homo sapiens

<400> 317

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Met Ser Gln Thr Gly Ser His Pro Gly Arg Gly Leu Ala Gly Arg
 1               5                  10                  15

Trp Leu Trp Gly Ala Gln Pro Cys Leu Leu Leu Pro Ile Val Pro
            20                  25                  30

Leu Ser Trp Leu Val Trp Leu Leu Leu Leu Leu Ala Ser Leu
            35                  40                  45

Leu Pro Ser Ala Arg Leu Ala Ser Pro Leu Pro Arg Glu Glu Glu
            50                  55                  60

Ile Val Phe Pro Glu Lys Leu Asn Gly Ser Val Leu Pro Gly Ser
            65                  70                  75

Gly Ala Pro Ala Arg Leu Leu Cys Arg Leu Gln Ala Phe Gly Glu
            80                  85                  90

Thr Leu Leu Leu Glu Leu Glu Gln Asp Ser Gly Val Gln Val Glu
            95                  100                 105

Gly Leu Thr Val Gln Tyr Leu Gly Gln Ala Pro Glu Leu Leu Gly
            110                 115                 120

Gly Ala Glu Pro Gly Thr Tyr Leu Thr Gly Thr Ile Asn Gly Asp
            125                 130                 135

Pro Glu Ser Val Ala Ser Leu His Trp Asp Gly Gly Ala Leu Leu
```

310

```
                    140                    145                    150

Gly Val Leu Gln Tyr Arg Gly Ala Glu Leu His Leu Gln Pro Leu
                155                    160                    165

Glu Gly Gly Thr Pro Asn Ser Ala Gly Gly Pro Gly Ala His Ile
                170                    175                    180

Leu Arg Arg Lys Ser Pro Ala Ser Gly Gln Gly Pro Met Cys Asn
                185                    190                    195

Val Lys Ala Pro Leu Gly Ser Pro Ser Pro Arg Pro Arg Arg Ala
                200                    205                    210

Lys Arg Phe Ala Ser Leu Ser Arg Phe Val Glu Thr Leu Val Val
                215                    220                    225

Ala Asp Asp Lys Met Ala Ala Phe His Gly Ala Gly Leu Lys Arg
                230                    235                    240

Tyr Leu Leu Thr Val Met Ala Ala Ala Lys Ala Phe Lys His
                245                    250                    255

Pro Ser Ile Arg Asn Pro Val Ser Leu Val Val Thr Arg Leu Val
                260                    265                    270

Ile Leu Gly Ser Gly Glu Glu Gly Pro Gln Val Gly Pro Ser Ala
                275                    280                    285

Ala Gln Thr Leu Arg Ser Phe Cys Ala Trp Gln Arg Gly Leu Asn
                290                    295                    300

Thr Pro Glu Asp Ser Gly Pro Asp His Phe Asp Thr Ala Ile Leu
                305                    310                    315

Phe Thr Arg Gln Asp Leu Cys Gly Val Ser Thr Cys Asp Thr Leu
                320                    325                    330

Gly Met Ala Asp Val Gly Thr Val Cys Asp Pro Ala Arg Ser Cys
                335                    340                    345

Ala Ile Val Glu Asp Asp Gly Leu Gln Ser Ala Phe Thr Ala Ala
                350                    355                    360

His Glu Leu Gly His Val Phe Asn Met Leu His Asp Asn Ser Lys
                365                    370                    375

Pro Cys Ile Ser Leu Asn Gly Pro Leu Ser Thr Ser Arg His Val
                380                    385                    390

Met Ala Pro Val Met Ala His Val Asp Pro Glu Glu Pro Trp Ser
                395                    400                    405

Pro Cys Ser Ala Arg Phe Ile Thr Asp Phe Leu Asp Asn Gly Tyr
                410                    415                    420

Gly His Cys Leu Leu Asp Lys Pro Glu Ala Pro Leu His Leu Pro
                425                    430                    435
```

311

```
Val Thr Phe Pro Gly Lys Asp Tyr Asp Ala Asp Arg Gln Cys Gln
                440             445                 450

Leu Thr Phe Gly Pro Asp Ser Arg His Cys Pro Gln Leu Pro Pro
                455             460                 465

Pro Cys Ala Ala Leu Trp Cys Ser Gly His Leu Asn Gly His Ala
                470             475                 480

Met Cys Gln Thr Lys His Ser Pro Trp Ala Asp Gly Thr Pro Cys
                485             490                 495

Gly Pro Ala Gln Ala Cys Met Gly Gly Arg Cys Leu His Met Asp
                500             505                 510

Gln Leu Gln Asp Phe Asn Ile Pro Gln Ala Gly Gly Trp Gly Pro
                515             520                 525

Trp Gly Pro Trp Gly Asp Cys Ser Arg Thr Cys Gly Gly Gly Val
                530             535                 540

Gln Phe Ser Ser Arg Asp Cys Thr Arg Pro Val Pro Arg Asn Gly
                545             550                 555

Gly Lys Tyr Cys Glu Gly Arg Arg Thr Arg Phe Arg Ser Cys Asn
                560             565                 570

Thr Glu Asp Cys Pro Thr Gly Ser Ala Leu Thr Phe Arg Glu Glu
                575             580                 585

Gln Cys Ala Ala Tyr Asn His Arg Thr Asp Leu Phe Lys Ser Phe
                590             595                 600

Pro Gly Pro Met Asp Trp Val Pro Arg Tyr Thr Gly Val Ala Pro
                605             610                 615

Gln Asp Gln Cys Lys Leu Thr Cys Gln Ala Arg Ala Leu Gly Tyr
                620             625                 630

Tyr Tyr Val Leu Glu Pro Arg Val Val Asp Gly Thr Pro Cys Ser
                635             640                 645

Pro Asp Ser Ser Ser Val Cys Val Gln Gly Arg Cys Ile His Ala
                650             655                 660

Gly Cys Asp Arg Ile Ile Gly Ser Lys Lys Lys Phe Asp Lys Cys
                665             670                 675

Met Val Cys Gly Gly Asp Gly Ser Gly Cys Ser Lys Gln Ser Gly
                680             685                 690

Ser Phe Arg Lys Phe Arg Tyr Gly Tyr Asn Asn Val Val Thr Ile
                695             700                 705

Pro Ala Gly Ala Thr His Ile Leu Val Arg Gln Gln Gly Asn Pro
                710             715                 720

Gly His Arg Ser Ile Tyr Leu Ala Leu Lys Leu Pro Asp Gly Ser
```

312

```
Tyr Ala Leu Asn Gly Glu Tyr Thr Leu Met Pro Ser Pro Thr Asp
            740                     745                 750

Val Val Leu Pro Gly Ala Val Ser Leu Arg Tyr Ser Gly Ala Thr
            755                     760                 765

Ala Ala Ser Glu Thr Leu Ser Gly His Gly Pro Leu Ala Gln Pro
            770                     775                 780

Leu Thr Leu Gln Val Leu Val Ala Gly Asn Pro Gln Asp Thr Arg
            785                     790                 795

Leu Arg Tyr Ser Phe Phe Val Pro Arg Pro Thr Pro Ser Thr Pro
            800                     805                 810

Arg Pro Thr Pro Gln Asp Trp Leu His Arg Arg Ala Gln Ile Leu
            815                     820                 825

Glu Ile Leu Arg Arg Arg Pro Trp Ala Gly Arg Lys
            830                     835
```

<210> 318
<211> 23
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-23
<223> Synthetic construct.

<400> 318
 ccctgaagct gccagatggc tcc 23

<210> 319
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 319
 ctgtgctctt cggtgcagcc agtc 24

<210> 320
<211> 43
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-43
<223> Synthetic construct.

<400> 320
ccacagatgt ggtactgcct ggggcagtca gcttgcgcta cag 43

<210> 321
<211> 1197
<212> DNA
<213> Homo sapiens

<400> 321
cagcagtggt ctctcagtcc tctcaaagca aggaaagagt actgtgtgct 50

gagagaccat ggcaaagaat cctccagaga attgtgaaga ctgtcacatt 100

ctaaatgcag aagctttaa atccaagaaa atatgtaaat cacttaagat 150

ttgtggactg gtgtttggta tcctggccct aactctaatt gtcctgtttt 200

gggggagcaa gcacttctgg ccggaggtac ccaaaaaagc ctatgacatg 250

gagcacactt tctacagcaa tggagagaag aagaagattt acatggaaat 300

tgatcctgtg accagaactg aaatattcag aagcggaaat ggcactgatg 350

aaacattgga agtgcacgac tttaaaaacg gatacactgg catctacttc 400

gtgggtcttc aaaaatgttt tatcaaaact cagattaaag tgattcctga 450

attttctgaa ccagaagagg aaatagatga gaatgaagaa attaccacaa 500

ctttctttga acagtcagtg atttgggtcc cagcagaaaa gcctattgaa 550

aaccgagatt ttcttaaaaa ttccaaaatt ctggagattt gtgataacgt 600

gaccatgtat tggatcaatc ccactctaat atcagtttct gagttacaag 650

actttgagga ggagggagaa gatcttcact ttcctgccaa cgaaaaaaaa 700

gggattgaac aaaatgaaca gtgggtggtc cctcaagtga agtagagaa 750

gacccgtcac gccagacaag caagtgagga agaacttcca ataaatgact 800

atactgaaaa tggaatagaa tttgatccca tgctggatga gagaggttat 850

tgttgtattt actgccgtcg aggcaaccgc tattgccgcc gcgtctgtga 900

acctttacta ggctactacc catatccata ctgctaccaa ggaggacgag 950

tcatctgtcg tgtcatcatg ccttgtaact ggtgggtggc ccgcatgctg 1000

gggagggtct aataggaggt ttgagctcaa atgcttaaac tgctggcaac 1050

atataataaa tgcatgctat tcaatgaatt tctgcctatg aggcatctgg 1100

cccctggtag ccagctctcc agaattactt gtaggtaatt cctctcttca 1150

tgttctaata aacttctaca ttatcaccaa aaaaaaaaaa aaaaaaa 1197

<210> 322

<211> 317
<212> PRT
<213> Homo sapiens

<400> 322
Met Ala Lys Asn Pro Pro Glu Asn Cys Glu Asp Cys His Ile Leu
 1   5   10   15

Asn Ala Glu Ala Phe Lys Ser Lys Lys Ile Cys Lys Ser Leu Lys
                20   25   30

Ile Cys Gly Leu Val Phe Gly Ile Leu Ala Leu Thr Leu Ile Val
                35   40   45

Leu Phe Trp Gly Ser Lys His Phe Trp Pro Glu Val Pro Lys Lys
                50   55   60

Ala Tyr Asp Met Glu His Thr Phe Tyr Ser Asn Gly Glu Lys Lys
                65   70   75

Lys Ile Tyr Met Glu Ile Asp Pro Val Thr Arg Thr Glu Ile Phe
                80   85   90

Arg Ser Gly Asn Gly Thr Asp Glu Thr Leu Glu Val His Asp Phe
                95   100   105

Lys Asn Gly Tyr Thr Gly Ile Tyr Phe Val Gly Leu Gln Lys Cys
                110   115   120

Phe Ile Lys Thr Gln Ile Lys Val Ile Pro Glu Phe Ser Glu Pro
                125   130   135

Glu Glu Glu Ile Asp Glu Asn Glu Glu Ile Thr Thr Thr Phe Phe
                140   145   150

Glu Gln Ser Val Ile Trp Val Pro Ala Glu Lys Pro Ile Glu Asn
                155   160   165

Arg Asp Phe Leu Lys Asn Ser Lys Ile Leu Glu Ile Cys Asp Asn
                170   175   180

Val Thr Met Tyr Trp Ile Asn Pro Thr Leu Ile Ser Val Ser Glu
                185   190   195

Leu Gln Asp Phe Glu Glu Glu Gly Glu Asp Leu His Phe Pro Ala
                200   205   210

Asn Glu Lys Lys Gly Ile Glu Gln Asn Glu Gln Trp Val Val Pro
                215   220   225

Gln Val Lys Val Glu Lys Thr Arg His Ala Arg Gln Ala Ser Glu
                230   235   240

Glu Glu Leu Pro Ile Asn Asp Tyr Thr Glu Asn Gly Ile Glu Phe
                245   250   255

Asp Pro Met Leu Asp Glu Arg Gly Tyr Cys Cys Ile Tyr Cys Arg
                260   265   270

315

Arg Gly Asn Arg Tyr Cys Arg Arg Val Cys Glu Pro Leu Leu Gly
            275   280   285

Tyr Tyr Pro Tyr Pro Tyr Cys Tyr Gln Gly Gly Arg Val Ile Cys
            290   295   300

Arg Val Ile Met Pro Cys Asn Trp Trp Val Ala Arg Met Leu Gly
            305   310   315

Arg Val

<210> 323
<211> 1174
<212> DNA
<213> Homo sapiens

<400> 323
gcggaactgg ctccggctgg cacctgagga gcggcgtgac cccgagggcc 50

cagggagctg cccggctggc ctaggcaggc agccgcacca tggccagcac 100

ggccgtgcag cttctgggct tcctgctcag cttcctgggc atggtgggca 150

cgttgatcac caccatcctg ccgcactggc ggaggacagc gcacgtgggc 200

accaacatcc tcacggccgt gtcctacctg aaagggctct ggatggagtg 250

tgtgtggcac agcacaggca tctaccagtg ccagatctac cgatccctgc 300

tggcgctgcc ccaagacctc caggctgccc gcgccctcat ggtcatctcc 350

tgcctgctct cgggcatagc ctgcgcctgc cgcgtcatcg ggatgaagtg 400

cacgcgctgc gccaagggca cacccgccaa gaccaccttt gccatcctcg 450

gcggcaccct cttcatcctg gccggcctcc tgtgcatggt ggccgtctcc 500

tggaccacca acgacgtggt gcagaacttc tacaacccgc tgctgcccag 550

cggcatgaag tttgagattg gccaggccct gtacctgggc ttcatctcct 600

cgtccctctc gctcattggt ggcaccctgc tttgcctgtc ctgccaggac 650

gaggcaccct acaggcccta ccaggccccg cccagggcca ccacgaccac 700

tgcaaacacc gcacctgcct accagccacc agctgcctac aaagacaatc 750

gggccccctc agtgacctcg gccacgcaca gcgggtacag gctgaacgac 800

tacgtgtgag tccccacagc ctgcttctcc cctgggctgc tgtgggctgg 850

gtccccggcg ggactgtcaa tggaggcagg ggttccagca caaagtttac 900

ttctgggcaa tttttgtatc caaggaaata atgtgaatgc gaggaaatgt 950

ctttagagca cagggacaga gggggaaata agaggaggag aaagctctct 1000

316

ataccaaaga ctgaaaaaaa aaatcctgtc tgtttttgta tttattatat 1050

atatttatgt gggtgatttg ataacaagtt taatataaag tgacttggga 1100

gtttggtcag tggggttggt ttgtgatcca ggaataaacc ttgcggatgt 1150

ggctgtttat gaaaaaaaaa aaaa 1174

<210> 324
<211> 239
<212> PRT
<213> Homo sapiens

<400> 324

```
Met Ala Ser Thr Ala Val Gln Leu Leu Gly Phe Leu Leu Ser Phe
 1               5                  10                  15

Leu Gly Met Val Gly Thr Leu Ile Thr Thr Ile Leu Pro His Trp
                20                  25                  30

Arg Arg Thr Ala His Val Gly Thr Asn Ile Leu Thr Ala Val Ser
                35                  40                  45

Tyr Leu Lys Gly Leu Trp Met Glu Cys Val Trp His Ser Thr Gly
                50                  55                  60

Ile Tyr Gln Cys Gln Ile Tyr Arg Ser Leu Leu Ala Leu Pro Gln
                65                  70                  75

Asp Leu Gln Ala Ala Arg Ala Leu Met Val Ile Ser Cys Leu Leu
                80                  85                  90

Ser Gly Ile Ala Cys Ala Cys Ala Val Ile Gly Met Lys Cys Thr
                95                  100                 105

Arg Cys Ala Lys Gly Thr Pro Ala Lys Thr Thr Phe Ala Ile Leu
                110                 115                 120

Gly Gly Thr Leu Phe Ile Leu Ala Gly Leu Leu Cys Met Val Ala
                125                 130                 135

Val Ser Trp Thr Thr Asn Asp Val Val Gln Asn Phe Tyr Asn Pro
                140                 145                 150

Leu Leu Pro Ser Gly Met Lys Phe Glu Ile Gly Gln Ala Leu Tyr
                155                 160                 165

Leu Gly Phe Ile Ser Ser Ser Leu Ser Leu Ile Gly Gly Thr Leu
                170                 175                 180

Leu Cys Leu Ser Cys Gln Asp Glu Ala Pro Tyr Arg Pro Tyr Gln
                185                 190                 195

Ala Pro Pro Arg Ala Thr Thr Thr Thr Ala Asn Thr Ala Pro Ala
                200                 205                 210

Tyr Gln Pro Pro Ala Ala Tyr Lys Asp Asn Arg Ala Pro Ser Val
                215                 220                 225
```

317

Thr Ser Ala Thr His Ser Gly Tyr Arg Leu Asn Asp Tyr Val
          230   235

<210> 325
<211> 2121
<212> DNA
<213> Homo sapiens

<400> 325
gagctcccct caggagcgcg ttagcttcac accttcggca gcaggagggc 50

ggcagcttct cgcaggcggc agggcgggcg gccaggatca tgtccaccac 100

cacatgccaa gtggtggcgt tcctcctgtc catcctgggg ctggccggct 150

gcatcgcggc caccgggatg gacatgtgga gcacccagga cctgtacgac 200

aaccccgtca cctccgtgtt ccagtacgaa gggctctgga ggagctgcgt 250

gaggcagagt tcaggcttca ccgaatgcag gccctatttc accatcctgg 300

gacttccagc catgctgcag gcagtgcgag ccctgatgat cgtaggcatc 350

gtcctgggtg ccattggcct cctggtatcc atctttgccc tgaaatgcat 400

ccgcattggc agcatggagg actctgccaa agccaacatg acactgacct 450

ccgggatcat gttcattgtc tcaggtcttt gtgcaattgc tggagtgtct 500

gtgtttgcca acatgctggt gactaacttc tggatgtcca cagctaacat 550

gtacaccggc atgggtggga tggtgcagac tgttcagacc aggtacacat 600

ttggtgcggc tctgttcgtg ggctgggtcg ctggaggcct cacactaatt 650

gggggtgtga tgatgtgcat cgcctgccgg ggcctggcac cagaagaaac 700

caactacaaa gccgtttctt atcatgcctc aggccacagt gttgcctaca 750

agcctggagg cttcaaggcc agcactggct ttgggtccaa caccaaaaac 800

aagaagatat acgatggagg tgcccgcaca gaggacgagg tacaatctta 850

tccttccaag cacgactatg tgtaatgctc taagacctct cagcacgggc 900

ggaagaaact cccggagagc tcacccaaaa acaaggaga tcccatctag 950

atttcttctt gctttttgact cacagctgga agttagaaaa gcctcgattt 1000

catctttgga gaggccaaat ggtcttagcc tcagtctctg tctctaaata 1050

ttccaccata aaacagctga gttatttatg aattagaggc tatagctcac 1100

attttcaatc ctctatttct tttttttaaat ataactttct actctgatga 1150

gagaatgtgg ttttaatctc tctctcacat tttgatgatt tagacagact 1200

ccccctcttc ctcctagtca ataaacccat tgatgatcta tttcccagct 1250

318

```
tatccccaag aaaacttttg aaaggaaaga gtagacccaa agatgttatt 1300

ttctgctgtt tgaattttgt ctccccaccc ccaacttggc tagtaataaa 1350

cacttactga agaagaagca ataagagaaa gatatttgta atctctccag 1400

cccatgatct cggttttctt acactgtgat cttaaaagtt accaaaccaa 1450

agtcattttc agtttgaggc aaccaaacct ttctactgct gttgacatct 1500

tcttattaca gcaacaccat tctaggagtt tcctgagctc tccactggag 1550

tcctctttct gtcgcgggtc agaaattgtc cctagatgaa tgagaaaatt 1600

attttttta atttaagtcc taaatatagt taaaataaat aatgttttag 1650

taaaatgata cactatctct gtgaaatagc ctcacccta catgtggata 1700

gaaggaaatg aaaaaataat tgctttgaca ttgtctatat ggtactttgt 1750

aaagtcatgc ttaagtacaa attccatgaa aagctcacac ctgtaatcct 1800

agcactttgg gaggctgagg aggaaggatc acttgagccc agaagttcga 1850

gactagcctg ggcaacatgg agaagccctg tctctacaaa atacagagag 1900

aaaaaatcag ccagtcatgg tggcatacac ctgtagtccc agcattccgg 1950

gaggctgagg tgggaggatc acttgagccc agggaggttg gggctgcagt 2000

gagccatgat cacaccactg cactccagcc aggtgacata gcgagatcct 2050

gtctaaaaaa ataaaaaata aataatggaa cacagcaagt cctaggaagt 2100

aggttaaaac taattcttta a 2121
```

<210> 326
<211> 261
<212> PRT
<213> Homo sapiens

<400> 326

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Met Ser Thr Thr Thr Cys Gln Val Val Ala Phe Leu Leu Ser Ile
 1               5                  10                  15

Leu Gly Leu Ala Gly Cys Ile Ala Ala Thr Gly Met Asp Met Trp
                20                  25                  30

Ser Thr Gln Asp Leu Tyr Asp Asn Pro Val Thr Ser Val Phe Gln
                35                  40                  45

Tyr Glu Gly Leu Trp Arg Ser Cys Val Arg Gln Ser Ser Gly Phe
                50                  55                  60

Thr Glu Cys Arg Pro Tyr Phe Thr Ile Leu Gly Leu Pro Ala Met
                65                  70                  75

Leu Gln Ala Val Arg Ala Leu Met Ile Val Gly Ile Val Leu Gly
```

319

Ala Ile Gly Leu Leu Val Ser Ile Phe Ala Leu Lys Cys Ile Arg
                    95   100   105

Ile Gly Ser Met Glu Asp Ser Ala Lys Ala Asn Met Thr Leu Thr
                   110   115   120

Ser Gly Ile Met Phe Ile Val Ser Gly Leu Cys Ala Ile Ala Gly
                   125   130   135

Val Ser Val Phe Ala Asn Met Leu Val Thr Asn Phe Trp Met Ser
                   140   145   150

Thr Ala Asn Met Tyr Thr Gly Met Gly Gly Met Val Gln Thr Val
                   155   160   165

Gln Thr Arg Tyr Thr Phe Gly Ala Ala Leu Phe Val Gly Trp Val
                   170   175   180

Ala Gly Gly Leu Thr Leu Ile Gly Gly Val Met Met Cys Ile Ala
                   185   190   195

Cys Arg Gly Leu Ala Pro Glu Glu Thr Asn Tyr Lys Ala Val Ser
                   200   205   210

Tyr His Ala Ser Gly His Ser Val Ala Tyr Lys Pro Gly Gly Phe
                   215   220   225

Lys Ala Ser Thr Gly Phe Gly Ser Asn Thr Lys Asn Lys Lys Ile
                   230   235   240

Tyr Asp Gly Gly Ala Arg Thr Glu Asp Glu Val Gln Ser Tyr Pro
                   245   250   255

Ser Lys His Asp Tyr Val
                   260

<210> 327
<211> 2010
<212> DNA
<213> Homo sapiens

<400> 327
 ggaaaaactg ttctcttctg tggcacagag aaccctgctt caaagcagaa 50

 gtagcagttc cggagtccag ctggctaaaa ctcatcccag aggataatgg 100

 caacccatgc cttagaaatc gctgggctgt ttcttggtgg tgttggaatg 150

 gtgggcacag tggctgtcac tgtcatgcct cagtggagag tgtcggcctt 200

 cattgaaaac aacatcgtgg tttttgaaaa cttctgggaa ggactgtgga 250

 tgaattgcgt gaggcaggct aacatcagga tgcagtgcaa aatctatgat 300

 tccctgctgg ctctttctcc ggacctacag gcagccagag gactgatgtg 350

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tgctgcttcc gtgatgtcct tcttggcttt catgatggcc atccttggca 400

tgaaatgcac caggtgcacg ggggacaatg agaaggtgaa ggctcacatt 450

ctgctgacgg ctggaatcat cttcatcatc acgggcatgg tggtgctcat 500

ccctgtgagc tgggttgcca atgccatcat cagagatttc tataactcaa 550

tagtgaatgt tgcccaaaaa cgtgagcttg gagaagctct ctacttagga 600

tggaccacgg cactggtgct gattgttgga ggagctctgt tctgctgcgt 650

ttttttgttgc aacgaaaaga gcagtagcta cagatactcg ataccttccc 700

atcgcacaac ccaaaaaagt tatcacaccg gaaagaagtc accgagcgtc 750

tactccagaa gtcagtatgt gtagttgtgt atgttttttt aactttacta 800

taaagccatg caaatgacaa aaatctatat tactttctca aaatggaccc 850

caaagaaact ttgatttact gttcttaact gcctaatctt aattacagga 900

actgtgcatc agctatttat gattctataa gctatttcag cagaatgaga 950

tattaaaccc aatgctttga ttgttctaga aagtatagta atttgttttc 1000

taaggtggtt caagcatcta ctctttttat catttacttc aaaatgacat 1050

tgctaaagac tgcattattt tactactgta atttctccac gacatagcat 1100

tatgtacata gatgagtgta acatttatat ctcacataga gacatgctta 1150

tatggtttta tttaaaatga aatgccagtc cattacactg aataaataga 1200

actcaactat tgcttttcag ggaaatcatg gatagggttg aagaaggtta 1250

ctattaattg tttaaaaaca gcttagggat taatgtcctc catttataat 1300

gaagattaaa atgaaggctt taatcagcat tgtaaaggaa attgaatggc 1350

tttctgatat gctgtttttt agcctaggag ttagaaatcc taacttcttt 1400

atcctcttct cccagaggct ttttttttct tgtgtattaa attaacattt 1450

ttaaaacgca gatattttgt caagggcttt gcattcaaa ctgctttttcc 1500

agggctatac tcagaagaaa gataaaagtg tgatctaaga aaaagtgatg 1550

gttttaggaa agtgaaaata ttttgttttt tgtatttgaa gaagaatgat 1600

gcattttgac aagaaatcat atatgtatgg atatatttta ataagtattt 1650

gagtacagac tttgaggttt catcaatata aataaaagag cagaaaaata 1700

tgtcttggtt ttcatttgct taccaaaaaa acaacaacaa aaaaagttgt 1750

cctttgagaa cttcacctgc tcctatgtgg gtacctgagt caaaattgtc 1800
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321

atttttgttc tgtgaaaaat aaatttcctt cttgtaccat ttctgtttag 1850

ttttactaaa atctgtaaat actgtatttt tctgtttatt ccaaatttga 1900

tgaaactgac aatccaattt gaaagtttgt gtcgacgtct gtctagctta 1950

aatgaatgtg ttctatttgc tttatacatt tatattaata aattgtacat 2000

ttttctaatt 2010

<210> 328
<211> 225
<212> PRT
<213> Homo sapiens

<400> 328

```
Met Ala Thr His Ala Leu Glu Ile Ala Gly Leu Phe Leu Gly Gly
  1               5                  10                  15

Val Gly Met Val Gly Thr Val Ala Val Thr Val Met Pro Gln Trp
                 20                  25                  30

Arg Val Ser Ala Phe Ile Glu Asn Asn Ile Val Val Phe Glu Asn
                 35                  40                  45

Phe Trp Glu Gly Leu Trp Met Asn Cys Val Arg Gln Ala Asn Ile
                 50                  55                  60

Arg Met Gln Cys Lys Ile Tyr Asp Ser Leu Leu Ala Leu Ser Pro
                 65                  70                  75

Asp Leu Gln Ala Ala Arg Gly Leu Met Cys Ala Ala Ser Val Met
                 80                  85                  90

Ser Phe Leu Ala Phe Met Met Ala Ile Leu Gly Met Lys Cys Thr
                 95                 100                 105

Arg Cys Thr Gly Asp Asn Glu Lys Val Lys Ala His Ile Leu Leu
                110                 115                 120

Thr Ala Gly Ile Ile Phe Ile Ile Thr Gly Met Val Val Leu Ile
                125                 130                 135

Pro Val Ser Trp Val Ala Asn Ala Ile Ile Arg Asp Phe Tyr Asn
                140                 145                 150

Ser Ile Val Asn Val Ala Gln Lys Arg Glu Leu Gly Glu Ala Leu
                155                 160                 165

Tyr Leu Gly Trp Thr Thr Ala Leu Val Leu Ile Val Gly Gly Ala
                170                 175                 180

Leu Phe Cys Cys Val Phe Cys Cys Asn Glu Lys Ser Ser Ser Tyr
                185                 190                 195

Arg Tyr Ser Ile Pro Ser His Arg Thr Thr Gln Lys Ser Tyr His
                200                 205                 210
```

322

```
Thr Gly Lys Lys Ser Pro Ser Val Tyr Ser Arg Ser Gln Tyr Val
          215                 220                 225
```

<210> 329
<211> 1315
<212> DNA
<213> Homo sapiens

<400> 329

```
tcgccatggc ctctgccgga atgcagatcc tgggagtcgt cctgacactg 50

ctgggctggg tgaatggcct ggtctcctgt gccctgccca tgtggaaggt 100

gaccgctttc atcggcaaca gcatcgtggt ggcccaggtg gtgtgggagg 150

gcctgtggat gtcctgcgtg gtgcagagca ccggccagat gcagtgcaag 200

gtgtacgact cactgctggc gctgccacag gacctgcagg ctgcacgtgc 250

cctctgtgtc atcgccctcc ttgtggccct gttcggcttg ctggtctacc 300

ttgctggggc caagtgtacc acctgtgtgg aggagaagga ttccaaggcc 350

cgcctggtgc tcacctctgg gattgtcttt gtcatctcag gggtcctgac 400

gctaatcccc gtgtgctgga cggcgcatgc catcatccgg gacttctata 450

accccctggt ggctgaggcc caaaagcggg agctgggggc ctccctctac 500

ttgggctggg cggcctcagg ccttttgttg ctgggtgggg ggttgctgtg 550

ctgcacttgc ccctcggggg ggtcccaggg ccccagccat tacatggccc 600

gctactcaac atctgcccct gccatctctc ggggggccctc tgagtaccct 650

accaagaatt acgtctgacg tggaggggaa tgggggctcc gctggcgcta 700

gagccatcca gaagtggcag tgcccaacag ctttgggatg ggttcgtacc 750

ttttgtttct gcctcctgct attttttcttt tgactgagga tatttaaaat 800

tcatttgaaa actgagccaa ggtgttgact cagactctca cttaggctct 850

gctgtttctc acccttggat gatggagcca agagggggat gctttgagat 900

tctggatctt gacatgccca tcttagaagc cagtcaagct atggaactaa 950

tgcggaggct gcttgctgtg ctggctttgc aacaagacag actgtcccca 1000

agagttcctg ctgctgctgg gggctgggct ccctagatg tcactggaca 1050

gctgcccccc atcctactca ggtctctgga gctcctctct tcacccctgg 1100

aaaaacaaat catctgttaa caaaggactg cccacctccg gaacttctga 1150

cctctgtttc ctccgtcctg ataagacgtc cacccccccag ggccaggtcc 1200

cagctatgta gacccccgcc cccacctcca acactgcacc cttctgccct 1250
```

323

gcccccctcg tctcacccccc tttacactca catttttatc aaataaagca 1300

tgttttgtta gtgca 1315

<210> 330
<211> 220
<212> PRT
<213> Homo sapiens

<400> 330

```
Met Ala Ser Ala Gly Met Gln Ile Leu Gly Val Val Leu Thr Leu
 1               5                  10                  15

Leu Gly Trp Val Asn Gly Leu Val Ser Cys Ala Leu Pro Met Trp
                20                  25                  30

Lys Val Thr Ala Phe Ile Gly Asn Ser Ile Val Val Ala Gln Val
                35                  40                  45

Val Trp Glu Gly Leu Trp Met Ser Cys Val Val Gln Ser Thr Gly
                50                  55                  60

Gln Met Gln Cys Lys Val Tyr Asp Ser Leu Leu Ala Leu Pro Gln
                65                  70                  75

Asp Leu Gln Ala Ala Arg Ala Leu Cys Val Ile Ala Leu Leu Val
                80                  85                  90

Ala Leu Phe Gly Leu Leu Val Tyr Leu Ala Gly Ala Lys Cys Thr
                95                  100                 105

Thr Cys Val Glu Glu Lys Asp Ser Lys Ala Arg Leu Val Leu Thr
                110                 115                 120

Ser Gly Ile Val Phe Val Ile Ser Gly Val Leu Thr Leu Ile Pro
                125                 130                 135

Val Cys Trp Thr Ala His Ala Ile Ile Arg Asp Phe Tyr Asn Pro
                140                 145                 150

Leu Val Ala Glu Ala Gln Lys Arg Glu Leu Gly Ala Ser Leu Tyr
                155                 160                 165

Leu Gly Trp Ala Ala Ser Gly Leu Leu Leu Leu Gly Gly Gly Leu
                170                 175                 180

Leu Cys Cys Thr Cys Pro Ser Gly Gly Ser.Gln Gly Pro Ser His
                185                 190                 195

Tyr Met Ala Arg Tyr Ser Thr Ser Ala Pro Ala Ile Ser Arg Gly
                200                 205                 210

Pro Ser Glu Tyr Pro Thr Lys Asn Tyr Val
                215                 220
```

<210> 331
<211> 1160
<212> DNA

324

<213> Homo sapiens

<400> 331
```
gccaaggaga acatcatcaa agacttctct agactcaaaa ggcttccacg 50

ttctacatct tgagcatctt ctaccactcc gaattgaacc agtcttcaaa 100

gtaaaggcaa tggcatttta tcccttgcaa attgctgggc tggttcttgg 150

gttccttggc atggtgggga ctcttgccac aacccttctg cctcagtggt 200

ggagtatcag cttttgttgg cagcaacatt attgtctttg agaggctctg 250

ggaagggctc tggatgaatt gcatccgaca agccagggtc cggttgcaat 300

gcaagttcta tagctccttg ttggctctcc cgcctgccct ggaaacagcc 350

cgggccctca tgtgtgtggc tgttgctctc tccttgatcg ccctgcttat 400

tggcatctgt ggcatgaagc aggtccagtg cacaggctct aacgagaggg 450

ccaaagcata ccttctggga acttcaggag tcctcttcat cctgacgggt 500

atcttcgttc tgattccggt gagctggaca gccaatataa tcatcagaga 550

tttctacaac ccagccatcc acataggtca gaaacgagag ctgggagcag 600

cacttttcct tggctgggca agcgctgctg tcctcttcat tggagggggt 650

ctgctttgtg dattttgctg ctgcaacaga aagaagcaag ggtacagata 700

tccagtgcct ggctaccgtg tgccacacac agataagcga agaaatacga 750

caatgcttag taagacctcc accagttatg tctaatgcct ccttttggct 800

ccaagtatgg actatggtca atgttttta taaagtcctg ctagaaactg 850

taagtatgtg aggcaggaga acttgcttta tgtctagatt tacattgata 900

cgaaagtttc aatttgttac tggtggtagg aatgaaaatg acttacttgg 950

acattctgac ttcaggtgta ttaaatgcat tgactattgt tggacccaat 1000

cgctgctcca attttcatat tctaaattca agtatacccaa taatcattag 1050

caagtgtaca atgatggact acttattact ttttgaccat catgtattat 1100

ctgataagaa tctaaagttg aaattgatat tctataacaa taaaacatat 1150

acctattcta 1160
```

<210> 332
<211> 173
<212> PRT
<213> Homo sapiens

<400> 332
Met Asn Cys Ile Arg Gln Ala Arg Val Arg Leu Gln Cys Lys Phe

325

```
        1                   5                   10                   15
     Tyr Ser Ser Leu Leu Ala Leu Pro Pro Ala Leu Glu Thr Ala Arg
                     20                  25                  30

     Ala Leu Met Cys Val Ala Val Ala Leu Ser Leu Ile Ala Leu Leu
                     35                  40                  45

     Ile Gly Ile Cys Gly Met Lys Gln Val Gln Cys Thr Gly Ser Asn
                     50                  55                  60

     Glu Arg Ala Lys Ala Tyr Leu Leu Gly Thr Ser Gly Val Leu Phe
                     65                  70                  75

     Ile Leu Thr Gly Ile Phe Val Leu Ile Pro Val Ser Trp Thr Ala
                     80                  85                  90

     Asn Ile Ile Ile Arg Asp Phe Tyr Asn Pro Ala Ile His Ile Gly
                     95                  100                 105

     Gln Lys Arg Glu Leu Gly Ala Ala Leu Phe Leu Gly Trp Ala Ser
                     110                 115                 120

     Ala Ala Val Leu Phe Ile Gly Gly Gly Leu Leu Cys Gly Phe Cys
                     125                 130                 135

     Cys Cys Asn Arg Lys Lys Gln Gly Tyr Arg Tyr Pro Val Pro Gly
                     140                 145                 150

     Tyr Arg Val Pro His Thr Asp Lys Arg Arg Asn Thr Thr Met Leu
                     155                 160                 165

     Ser Lys Thr Ser Thr Ser Tyr Val
                     170
```

<210> 333
<211> 535
<212> DNA
<213> Homo sapiens

<400> 333
```
agtgacaatc tcagagcagc ttctacacca cagccatttc cagcatgaag  50

atcactgggg gtctccttct gctctgtaca gtggtctatt tctgtagcag  100

ctcagaagct gctagtctgt ctccaaaaaa agtggactgc agcatttaca  150

agaagtatcc agtggtggcc atcccctgcc ccatcacata cctaccagtt  200

tgtggttctg actacatcac ctatgggaat gaatgtcact tgtgtaccga  250

gagcttgaaa agtaatggaa gagttcagtt tcttcacgat ggaagttgct  300

aaattctcca tggacataga gagaaaggaa tgatattctc atcatcatct  350

tcatcatccc aggctctgac tgagtttctt tcagtttttac tgatgttctg  400

ggtgggggac agagccagat tcagagtaat cttgactgaa tggagaaagt  450
```

ttctgtgcta cccctacaaa cccatgcctc actgacagac cagcattttt 500

tttttaacac gtcaataaaa aaataatctc ccaga 535

<210> 334
<211> 85
<212> PRT
<213> Homo sapiens

<400> 334
```
Met Lys Ile Thr Gly Gly Leu Leu Leu Leu Cys Thr Val Val Tyr
 1               5                  10                  15

Phe Cys Ser Ser Ser Glu Ala Ala Ser Leu Ser Pro Lys Lys Val
                20                  25                  30

Asp Cys Ser Ile Tyr Lys Lys Tyr Pro Val Val Ala Ile Pro Cys
                35                  40                  45

Pro Ile Thr Tyr Leu Pro Val Cys Gly Ser Asp Tyr Ile Thr Tyr
                50                  55                  60

Gly Asn Glu Cys His Leu Cys Thr Glu Ser Leu Lys Ser Asn Gly
                65                  70                  75

Arg Val Gln Phe Leu His Asp Gly Ser Cys
                80                  85
```

<210> 335
<211> 742
<212> DNA
<213> Homo sapiens

<400> 335

cccgcgcccg gttctccctc gcagcacctc gaagtgcgcc cctcgccctc 50

ctgctcgcgc cccgccgcca tggctgcctc ccccgcgcgg cctgctgtcc 100

tggccctgac cgggctggcg ctgctcctgc tcctgtgctg gggcccaggt 150

ggcataagtg gaaataaact caagctgatg cttcaaaaac gagaagcacc 200

tgttccaact aagactaaag tggccgttga tgagaataaa gccaaagaat 250

tccttggcag cctgaagcgc cagaagcggc agctgtggga ccggactcgg 300

cccgaggtgc agcagtggta ccagcagttt ctctacatgg ctttgatga 350

agcgaaattt gaagatgaca tcacctattg gcttaacaga gatcgaaatg 400

gacatgaata ctatggcgat tactaccaac gtcactatga tgaagactct 450

gcaattggtc cccggagccc ctacggcttt aggcatggag ccagcgtcaa 500

ctacgatgac tactaaccat gacttgccac acgctgtaca agaagcaaat 550

agcgattctc ttcatgtatc tcctaatgcc ttacactact tggtttctga 600

```
tttgctctat ttcagcagat cttttctacc tactttgtgt gatcaaaaaa 650

gaagagttaa aacaacacat gtaaatgcct tttgatattt catgggaatg 700

cctctcattt aaaaatagaa ataaagcatt ttgttaaaaa ga 742
```

<210> 336
<211> 148
<212> PRT
<213> Homo sapiens

<400> 336

```
Met Ala Ala Ser Pro Ala Arg Pro Ala Val Leu Ala Leu Thr Gly
 1               5                  10                  15

Leu Ala Leu Leu Leu Leu Leu Cys Trp Gly Pro Gly Gly Ile Ser
              20                  25                  30

Gly Asn Lys Leu Lys Leu Met Leu Gln Lys Arg Glu Ala Pro Val
              35                  40                  45

Pro Thr Lys Thr Lys Val Ala Val Asp Glu Asn Lys Ala Lys Glu
              50                  55                  60

Phe Leu Gly Ser Leu Lys Arg Gln Lys Arg Gln Leu Trp Asp Arg
              65                  70                  75

Thr Arg Pro Glu Val Gln Gln Trp Tyr Gln Gln Phe Leu Tyr Met
              80                  85                  90

Gly Phe Asp Glu Ala Lys Phe Glu Asp Asp Ile Thr Tyr Trp Leu
              95                  100                 105

Asn Arg Asp Arg Asn Gly His Glu Tyr Tyr Gly Asp Tyr Tyr Gln
              110                 115                 120

Arg His Tyr Asp Glu Asp Ser Ala Ile Gly Pro Arg Ser Pro Tyr
              125                 130                 135

Gly Phe Arg His Gly Ala Ser Val Asn Tyr Asp Asp Tyr
              140                 145
```

<210> 337
<211> 1310
<212> DNA
<213> Homo sapiens

<400> 337

```
cggctcgagc ccgcccggaa gtgcccgagg ggccgcgatg gagctggggg 50

agccgggcgc tcggtagcgc ggcgggcaag gcaggcgcca tgaccctgat 100

tgaaggggtg ggtgatgagg tgaccgtcct tttctcggtg cttgcctgcc 150

ttctggtgct ggcccttgcc tgggtctcaa cgcacaccgc tgagggcggg 200

gacccactgc cccagccgtc agggacccca acgccatccc agcccagcgc 250
```

328

```
agccatggca gctaccgaca gcatgagagg ggaggcccca ggggcagaga 300

cccccagcct gagacacaga ggtcaagctg cacagccaga gcccagcacg 350

gggttcacag caacaccgcc agccccggac tccccgcagg agcccctcgt 400

gctacggctg aaattcctca atgattcaga gcaggtggcc agggcctggc 450

cccacgacac cattggctcc ttgaaaagga cccagtttcc cggccgggaa 500

cagcaggtgc gactcatcta ccaagggcag ctgctaggcg acgacaccca 550

gaccctgggc agccttcacc tccctcccaa ctgcgttctc cactgccacg 600

tgtccacgag agtcggtccc ccaaatcccc cctgcccgcc ggggtccgag 650

cccggcccct ccgggctgga aatcggcagc ctgctgctgc ccctgctgct 700

cctgctgttg ctgctgctct ggtactgcca gatccagtac cggcccttct 750

ttcccctgac cgccactctg ggcctggccg gcttcaccct gctcctcagt 800

ctcctggcct ttgccatgta ccgcccgtag tgcctccgcg ggcgcttggc 850

agcgtcgccg gcccctccgg accttgctcc ccgcgccgcg gcgggagctg 900

ctgcctgccc aggcccgcct ctccggcctg cctcttcccg ctgccctgga 950

gcccagccct cgccgcagga ggactcccgg gactggcgga ggccccgccc 1000

tgcgaccgcc ggggctcggg gccacctccc ggggctgctg aacctcagcc 1050

cgcactggga gtgggctcct cggggtcggg catctgctgt cgctgcctcg 1100

gccccgggca gagccgggcc gccccggggg cccgtcttag tgttctgccg 1150

gaggacccag ccgcctccaa tccctgacag ctccttgggc tgagttgggg 1200

acgccaggtc ggtgggaggc tggtgaaggg gagcggggag gggcagagga 1250

gttccccgga acccgtgcag attaaagtaa ctgtgaagtt ttaaaaaaaa 1300

aaaaaaaaaa 1310
```

<210> 338
<211> 246
<212> PRT
<213> Homo sapiens

<400> 338
```
Met Thr Leu Ile Glu Gly Val Gly Asp Glu Val Thr Val Leu Phe
 1               5                  10                  15

Ser Val Leu Ala Cys Leu Leu Val Leu Ala Leu Ala Trp Val Ser
                20                  25                  30

Thr His Thr Ala Glu Gly Gly Asp Pro Leu Pro Gln Pro Ser Gly
                35                  40                  45
```

329

```
Thr Pro Thr Pro Ser Gln Pro Ser Ala Ala Met Ala Ala Thr Asp
                50                  55                  60

Ser Met Arg Gly Glu Ala Pro Gly Ala Glu Thr Pro Ser Leu Arg
                65                  70                  75

His Arg Gly Gln Ala Ala Gln Pro Glu Pro Ser Thr Gly Phe Thr
                80                  85                  90

Ala Thr Pro Pro Ala Pro Asp Ser Pro Gln Glu Pro Leu Val Leu
                95                  100                 105

Arg Leu Lys Phe Leu Asn Asp Ser Glu Gln Val Ala Arg Ala Trp
                110                 115                 120

Pro His Asp Thr Ile Gly Ser Leu Lys Arg Thr Gln Phe Pro Gly
                125                 130                 135

Arg Glu Gln Gln Val Arg Leu Ile Tyr Gln Gly Gln Leu Leu Gly
                140                 145                 150

Asp Asp Thr Gln Thr Leu Gly Ser Leu His Leu Pro Pro Asn Cys
                155                 160                 165

Val Leu His Cys His Val Ser Thr Arg Val Gly Pro Pro Asn Pro
                170                 175                 180

Pro Cys Pro Pro Gly Ser Glu Pro Gly Pro Ser Gly Leu Glu Ile
                185                 190                 195

Gly Ser Leu Leu Leu Pro Leu Leu Leu Leu Leu Leu Leu Leu Leu
                200                 205                 210

Trp Tyr Cys Gln Ile Gln Tyr Arg Pro Phe Phe Pro Leu Thr Ala
                215                 220                 225

Thr Leu Gly Leu Ala Gly Phe Thr Leu Leu Leu Ser Leu Leu Ala
                230                 235                 240

Phe Ala Met Tyr Arg Pro
                245

<210> 339
<211> 849
<212> DNA
<213> Homo sapiens

<400> 339
gagattggaa acagccaggt tggagcagtg agtgagtaag gaaacctggc 50

tgccctctcc agattcccca ggctctcaga gaagatcagc agaaagtctg 100

caagacccta agaaccatca gccctcagct gcacctcctc ccctccaagg 150

atgacaaagg cgctactcat ctatttggtc agcagctttc ttgccctaaa 200

tcaggccagc ctcatcagtc gctgtgactt ggcccaggtg ctgcagctgg 250
```

330

```
aggacttgga tggtttgag ggttactccc tgagtgactg gctgtgcctg 300

gcttttgtgg aaagcaagtt caacatatca aagataaatg aaaatgcgga 350

tggaagcttt gactatggcc tcttccagat caacagccac tactggtgca 400

acgattataa gagttactcg gaaaaccttt gccacgtaga ctgtcaagat 450

ctgctgaatc ccaaccttct tgcaggcatc cactgcgcaa aaaggattgt 500

gtccggagca cggggggatga caactgggt agaatggagg ttgcactgtt 550

caggccggcc actctcctac tggctgacag gatgccgcct gagatgaaac 600

agggtgcggg tgcaccgtgg agtcattcca agactcctgt cctcactcag 650

ggattcttca tttcttcttc ctactgcctc cacttcatgt tattttcttc 700

ccttcccatt tacaactaaa actgaccaga gccccaggaa taaatggttt 750

tcttggcttc ctccttactc ccatctggac ccagtccccct ggttcctgtc 800

tgttatttgt aaactgagga ccacaataaa gaaatcttta tatttatcg 849
```

<210> 340
<211> 148
<212> PRT
<213> Homo sapiens

<400> 340

```
Met Thr Lys Ala Leu Leu Ile Tyr Leu Val Ser Ser Phe Leu Ala
  1               5                  10                  15

Leu Asn Gln Ala Ser Leu Ile Ser Arg Cys Asp Leu Ala Gln Val
                 20                  25                  30

Leu Gln Leu Glu Asp Leu Asp Gly Phe Glu Gly Tyr Ser Leu Ser
                 35                  40                  45

Asp Trp Leu Cys Leu Ala Phe Val Glu Ser Lys Phe Asn Ile Ser
                 50                  55                  60

Lys Ile Asn Glu Asn Ala Asp Gly Ser Phe Asp Tyr Gly Leu Phe
                 65                  70                  75

Gln Ile Asn Ser His Tyr Trp Cys Asn Asp Tyr Lys Ser Tyr Ser
                 80                  85                  90

Glu Asn Leu Cys His Val Asp Cys Gln Asp Leu Leu Asn Pro Asn
                 95                 100                 105

Leu Leu Ala Gly Ile His Cys Ala Lys Arg Ile Val Ser Gly Ala
                110                 115                 120

Arg Gly Met Asn Asn Trp Val Glu Trp Arg Leu His Cys Ser Gly
                125                 130                 135

Arg Pro Leu Ser Tyr Trp Leu Thr Gly Cys Arg Leu Arg
```

331

<210> 341
<211> 23
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-23
<223> Synthetic construct.

<400> 341
 ccctccaagg atgacaaagg cgc 23

<210> 342
<211> 29
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-29
<223> Synthetic construct.

<400> 342
 ggtcagcagc tttcttgccc taaatcagg 29

<210> 343
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 343
 atctcaggcg gcatcctgtc agcc 24

<210> 344
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 344
 gtggatgcct gcaagaaggt tggg 24

<210> 345
<211> 45
<212> DNA
<213> Artificial

```
<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 345
agctttcttg ccctaaatca ggccagcctc atcagtcgct gtgac 45

<210> 346
<211> 2575
<212> DNA
<213> Homo sapiens

<400> 346
tctgacctga ctggaagcgt ccaaagaggg acggctgtca gccctgcttg 50

actgagaacc caccagctca tcccagacac ctcatagcaa cctatttata 100

caaagggggga aagaaacacc tgagcagaat ggaatcatta tttttttccc 150

aaggagaaaa ccggggtaaa gggagggaag caattcaatt tgaagtccct 200

gtgaatgggc tttcagaagg caattaaaga aatccactca gagaggactt 250

ggggtgaaac ttgggtcctg tggttttctg attgtaagtg gaagcaggtc 300

ttgcacacgc tgttggcaaa tgtcaggacc aggttaagtg actggcagaa 350

aaacttccag gtggaacaag caacccatgt tctgctgcaa gcttgaagga 400

gcctggagcg ggagaaagct aacttgaaca tgacctgttg catttggcaa 450

gttctagcaa catgctccta aggaagcgat acaggcacag accatgcaga 500

ctccagttcc tcctgctgct cctgatgctg ggatgcgtcc tgatgatggt 550

ggcgatgttg caccctcccc accacaccct gcaccagact gtcacagccc 600

aagccagcaa gcacagccct gaagccaggt accgcctgga ctttggggaa 650

tcccaggatt gggtactgga agctgaggat gagggtgaag agtacagccc 700

tctggagggc ctgccaccct ttatctcact gcgggaggat cagctgctgg 750

tggccgtggc cttaccccag gccagaagga accagagcca gggcaggaga 800

ggtgggagct accgcctcat caagcagcca aggaggcagg ataaggaagc 850

cccaaagagg gactgggggg ctgatgagga cggggaggtg tctgaagaag 900

aggagttgac cccgttcagc ctggacccac gtggcctcca ggaggcactc 950

agtgcccgca tccccctcca gagggctctg cccgaggtgc ggcacccact 1000

gtgtctgcag cagcaccctc aggacagcct gcccacagcc agcgtcatcc 1050

tctgtttcca tgatgaggcc tggtccactc tcctgcggac tgtacacagc 1100
```

333

```
atcctcgaca cagtgcccag ggccttcctg aaggagatca tcctcgtgga 1150

cgacctcagc cagcaaggac aactcaagtc tgctctcagc gaatatgtgg 1200

ccaggctgga gggggtgaag ttactcagga gcaacaagag gctgggtgcc 1250

atcagggccc ggatgctggg ggccaccaga gccaccgggg atgtgctcgt 1300

cttcatggat gcccactgcg agtgccaccc aggctggctg gagcccctcc 1350

tcagcagaat agctggtgac aggagccgag tggtatctcc ggtgatagat 1400

gtgattgact ggaagacttt ccagtattac ccctcaaagg acctgcagcg 1450

tggggtgttg gactggaagc tggatttcca ctgggaacct ttgccagagc 1500

atgtgaggaa ggccctccag tcccccataa gccccatcag gagccctgtg 1550

gtgcccggag aggtggtggc catggacaga cattacttcc aaaacactgg 1600

agcgtatgac tctcttatgt cgctgcgagg tggtgaaaac ctcgaactgt 1650

ctttcaaggc ctggctctgt ggtggctctg ttgaaatcct tccctgctct 1700

cgggtaggac acatctacca aaatcaggat tcccattccc ccctcgacca 1750

ggaggccacc ctgaggaaca gggttcgcat tgctgagacc tggctggggt 1800

cattcaaaga aaccttctac aagcatagcc cagaggcctt ctccttgagc 1850

aaggctgaga agccagactg catggaacgc ttgcagctgc aaaggagact 1900

gggttgtcgg acattccact ggtttctggc taatgtctac cctgagctgt 1950

acccatctga acccaggccc agtttctctg gaaagctcca caacactgga 2000

cttgggctct gtgcagactg ccaggcagaa ggggacatcc tgggctgtcc 2050

catggtgttg gctccttgca gtgacagccg gcagcaacag tacctgcagc 2100

acaccagcag gaaggagatt cactttggca gcccacagca cctgtgcttt 2150

gctgtcaggc aggagcaggt gattcttcag aactgcacgg aggaaggcct 2200

ggccatccac cagcagcact gggacttcca ggagaatggg atgattgtcc 2250

acattctttc tgggaaatgc atggaagctg tggtgcaaga aaacaataaa 2300

gatttgtacc tgcgtccgtg tgatggaaaa gcccgccagc agtggcgatt 2350

tgaccagata aatgctgtgg atgaacgatg aatgtcaatg tcagaaggaa 2400

aagagaattt tggccatcaa aatccagctc caagtgaacg taaagagctt 2450

atatatttca tgaagctgat cctttgtgt gtgtgctcct tgtgttagga 2500

gagaaaaaag ctctatgaaa gaatatagga agtttctcct tttcacacct 2550
```

334

tatttcattg actgctggct gctta 2575

<210> 347
<211> 639
<212> PRT
<213> Homo sapiens

<400> 347
```
Met Leu Leu Arg Lys Arg Tyr Arg His Arg Pro Cys Arg Leu Gln
  1               5                  10                  15

Phe Leu Leu Leu Leu Leu Met Leu Gly Cys Val Leu Met Met Val
               20                  25                  30

Ala Met Leu His Pro Pro His His Thr Leu His Gln Thr Val Thr
               35                  40                  45

Ala Gln Ala Ser Lys His Ser Pro Glu Ala Arg Tyr Arg Leu Asp
               50                  55                  60

Phe Gly Glu Ser Gln Asp Trp Val Leu Glu Ala Glu Asp Glu Gly
               65                  70                  75

Glu Glu Tyr Ser Pro Leu Glu Gly Leu Pro Pro Phe Ile Ser Leu
               80                  85                  90

Arg Glu Asp Gln Leu Leu Val Ala Val Ala Leu Pro Gln Ala Arg
               95                 100                 105

Arg Asn Gln Ser Gln Gly Arg Arg Gly Gly Ser Tyr Arg Leu Ile
              110                 115                 120

Lys Gln Pro Arg Arg Gln Asp Lys Glu Ala Pro Lys Arg Asp Trp
              125                 130                 135

Gly Ala Asp Glu Asp Gly Glu Val Ser Glu Glu Glu Leu Thr
              140                 145                 150

Pro Phe Ser Leu Asp Pro Arg Gly Leu Gln Glu Ala Leu Ser Ala
              155                 160                 165

Arg Ile Pro Leu Gln Arg Ala Leu Pro Glu Val Arg His Pro Leu
              170                 175                 180

Cys Leu Gln Gln His Pro Gln Asp Ser Leu Pro Thr Ala Ser Val
              185                 190                 195

Ile Leu Cys Phe His Asp Glu Ala Trp Ser Thr Leu Leu Arg Thr
              200                 205                 210

Val His Ser Ile Leu Asp Thr Val Pro Arg Ala Phe Leu Lys Glu
              215                 220                 225

Ile Ile Leu Val Asp Asp Leu Ser Gln Gln Gly Gln Leu Lys Ser
              230                 235                 240

Ala Leu Ser Glu Tyr Val Ala Arg Leu Glu Gly Val Lys Leu Leu
              245                 250                 255
```

335

```
Arg Ser Asn Lys Arg Leu Gly Ala Ile Arg Ala Arg Met Leu Gly
            260             265             270

Ala Thr Arg Ala Thr Gly Asp Val Leu Val Phe Met Asp Ala His
            275             280             285

Cys Glu Cys His Pro Gly Trp Leu Glu Pro Leu Leu Ser Arg Ile
            290             295             300

Ala Gly Asp Arg Ser Arg Val Val Ser Pro Val Ile Asp Val Ile
            305             310             315

Asp Trp Lys Thr Phe Gln Tyr Tyr Pro Ser Lys Asp Leu Gln Arg
            320             325             330

Gly Val Leu Asp Trp Lys Leu Asp Phe His Trp Glu Pro Leu Pro
            335             340             345

Glu His Val Arg Lys Ala Leu Gln Ser Pro Ile Ser Pro Ile Arg
            350             355             360

Ser Pro Val Val Pro Gly Glu Val Val Ala Met Asp Arg His Tyr
            365             370             375

Phe Gln Asn Thr Gly Ala Tyr Asp Ser Leu Met Ser Leu Arg Gly
            380             385             390

Gly Glu Asn Leu Glu Leu Ser Phe Lys Ala Trp Leu Cys Gly Gly
            395             400             405

Ser Val Glu Ile Leu Pro Cys Ser Arg Val Gly His Ile Tyr Gln
            410             415             420

Asn Gln Asp Ser His Ser Pro Leu Asp Gln Glu Ala Thr Leu Arg
            425             430             435

Asn Arg Val Arg Ile Ala Glu Thr Trp Leu Gly Ser Phe Lys Glu
            440             445             450

Thr Phe Tyr Lys His Ser Pro Glu Ala Phe Ser Leu Ser Lys Ala
            455             460             465

Glu Lys Pro Asp Cys Met Glu Arg Leu Gln Leu Gln Arg Arg Leu
            470             475             480

Gly Cys Arg Thr Phe His Trp Phe Leu Ala Asn Val Tyr Pro Glu
            485             490             495

Leu Tyr Pro Ser Glu Pro Arg Pro Ser Phe Ser Gly Lys Leu His
            500             505             510

Asn Thr Gly Leu Gly Leu Cys Ala Asp Cys Gln Ala Glu Gly Asp
            515             520             525

Ile Leu Gly Cys Pro Met Val Leu Ala Pro Cys Ser Asp Ser Arg
            530             535             540

Gln Gln Gln Tyr Leu Gln His Thr Ser Arg Lys Glu Ile His Phe
```

336

```
                545                      550                      555
   Gly Ser Pro Gln His Leu Cys Phe Ala Val Arg Gln Glu Gln Val
               560                      565                      570

   Ile Leu Gln Asn Cys Thr Glu Glu Gly Leu Ala Ile His Gln Gln
               575                      580                      585

   His Trp Asp Phe Gln Glu Asn Gly Met Ile Val His Ile Leu Ser
               590                      595                      600

   Gly Lys Cys Met Glu Ala Val Val Gln Glu Asn Asn Lys Asp Leu
               605                      610                      615

   Tyr Leu Arg Pro Cys Asp Gly Lys Ala Arg Gln Gln Trp Arg Phe
               620                      625                      630

   Asp Gln Ile Asn Ala Val Asp Glu Arg
               635
```

```
<210> 348
<211> 23
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-23
<223> Synthetic construct.

<400> 348
 ggagaggtgg tggccatgga cag 23

<210> 349
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 349
 ctgtcactgc aaggagccaa cacc 24

<210> 350
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 350
 tatgtcgctg cgaggtggtg aaaacctcga actgtctttc aaggc 45
```

<210> 351
<211> 2524
<212> DNA
<213> Homo sapiens

<400> 351
cgccaagcat gcagtaaagg ctgaaaatct gggtcacagc tgaggaagac 50

ctcagacatg gagtccagga tgtggcctgc gctgctgctg tcccacctcc 100

tccctctctg gccactgctg ttgctgcccc tcccaccgcc tgctcagggc 150

tcttcatcct ccccctcgaac cccaccagcc ccagcccgcc ccccgtgtgc 200

cagggaggc ccctcggccc cacgtcatgt gtgcgtgtgg gagcgagcac 250

ctccaccaag ccgatctcct cgggtcccaa gatcacgtcg gcaagtcctg 300

cctggcactg cacccccagc caccccatca ggctttgagg aggggccgcc 350

ctcatcccaa taccctgggg ctatcgtgtg gggtcccacc gtgtctcgag 400

aggatggagg ggaccccaac tctgccaatc ccggatttct ggactatggt 450

tttgcagccc ctcatgggct cgcaacccca caccccaact cagactccat 500

gcgaggtgat ggagatgggc ttatccttgg agaggcacct gccaccctgc 550

ggccattcct gttcggggggc cgtggggaag gtgtggaccc ccagctctat 600

gtcacaatta ccatctccat catcattgtt ctcgtggcca ctggcatcat 650

cttcaagttc tgctgggacc gcagccagaa gcgacgcaga ccctcagggc 700

agcaaggtgc cctgaggcag gaggagagcc agcagccact gacagacctg 750

tccccggctg gagtcactgt gctggggggcc ttcggggact cacctacccc 800

cacccctgac catgaggagc cccgaggggg accccggcct gggatgcccc 850

accccaaggg ggctccagcc ttccagttga accggtgagg gcaggggcaa 900

tgggatggga gggcaaagag ggaaggcaac ttaggtcttc agagctgggg 950

tggggggtgcc ctctggatgg gtagtgagga ggcaggcgtg gcctcccaca 1000

gcccctggcc ctcccaaggg ggctggacca gctcctctct gggaggcacc 1050

cttccttctc ccagtctctc aggatctgtg tcctattctc tgctgcccat 1100

aactccaact ctgccctctt tggttttttc tcatgccacc ttgtctaaga 1150

caactctgcc ctcttaacct tgattccccc tctttgtctt gaacttcccc 1200

ttctattctg gcctacccct tggttcctga ctgtgccctt tccctcttcc 1250

tctcaggatt cccctggtga atctgtgatg cccccaatgt tggggtgcag 1300

```
ccaagcagga ggccaagggg ccggcacagc ccccatccca ctgagggtgg 1350

ggcagctgtg gggagctggg gccacagggg ctcctggctc ctgccccttg 1400

cacaccaccc ggaacactcc ccagccccac gggcaatcct atctgctcgc 1450

cctcctgcag gtgggggcct cacatatctg tgacttcggg tccctgtccc 1500

caccccttgtg cactcacatg aaagccttgc acactcacct ccaccttcac 1550

aggccatttg cacacgctcc tgcaccctct ccccgtccat accgctccgc 1600

tcagctgact ctcatgttct ctcgtctcac atttgcactc tctccttccc 1650

acattctgtg ctcagctcac tcagtggtca gcgtttcctg cacactttac 1700

ctctcatgtg cgtttcccgg cctgatgttg tggtggtgtg cggcgtgctc 1750

actctctccc tcatgaacac ccacccacct cgtttccgca gcccctgcgt 1800

gctgctccag aggtgggtgg gaggtgagct gggggctcct tgggccctca 1850

tcggtcatgg tctcgtccca ttccacacca tttgtttctc tgtctcccca 1900

tcctactcca aggatgccgg catcaccctg agggctcccc cttgggaatg 1950

gggtagtgag gccccagact tcacccccag cccactgcta aaatctgttt 2000

tctgacagat gggttttggg gagtcgcctg ctgcactaca tgagaaaggg 2050

actcccattt gcccttccct ttctcctaca gtcccttttg tcttgtctgt 2100

cctggctgtc tgtgtgtgtg ccattctctg gacttcagag cccccctgagc 2150

cagtcctccc ttcccagcct ccctttgggc ctccctaact ccacctaggc 2200

tgccagggac cggagtcagc tggttcaagg ccatcgggag ctctgcctcc 2250

aagtctaccc ttcccttccc ggactccctc ctgtcccctc ctttcctccc 2300

tccttccttc cactctcctt ccttttgctt ccctgccctt tcccctcct 2350

caggttcttc cctccttctc actggttttt ccaccttcct ccttcccttc 2400

ttccctggct cctaggctgt gatatatatt tttgtattat ctctttcttc 2450

ttcttgtggt gatcatcttg aattactgtg ggatgtaagt ttcaaaattt 2500

tcaaataaag cctttgcaag ataa 2524
```

<210> 352
<211> 243
<212> PRT
<213> Homo sapiens

<400> 352
Met Arg Pro Gln Gly Pro Ala Ala Ser Pro Gln Arg Leu Arg Gly
 1   5   10   15

339

```
Leu Leu Leu Leu Leu Leu Leu Gln Leu Pro Ala Pro Ser Ser Ala
              20                  25                  30

Ser Glu Ile Pro Lys Gly Lys Gln Lys Ala Gln Leu Arg Gln Arg
              35                  40                  45

Glu Val Val Asp Leu Tyr Asn Gly Met Cys Leu Gln Gly Pro Ala
              50                  55                  60

Gly Val Pro Gly Arg Asp Gly Ser Pro Gly Ala Asn Val Ile Pro
              65                  70                  75

Gly Thr Pro Gly Ile Pro Gly Arg Asp Gly Phe Lys Gly Glu Lys
              80                  85                  90

Gly Glu Cys Leu Arg Glu Ser Phe Glu Glu Ser Trp Thr Pro Asn
              95                 100                 105

Tyr Lys Gln Cys Ser Trp Ser Ser Leu Asn Tyr Gly Ile Asp Leu
             110                 115                 120

Gly Lys Ile Ala Glu Cys Thr Phe Thr Lys Met Arg Ser Asn Ser
             125                 130                 135

Ala Leu Arg Val Leu Phe Ser Gly Ser Leu Arg Leu Lys Cys Arg
             140                 145                 150

Asn Ala Cys Cys Gln Arg Trp Tyr Phe Thr Phe Asn Gly Ala Glu
             155                 160                 165

Cys Ser Gly Pro Leu Pro Ile Glu Ala Ile Ile Tyr Leu Asp Gln
             170                 175                 180

Gly Ser Pro Glu Met Asn Ser Thr Ile Asn Ile His Arg Thr Ser
             185                 190                 195

Ser Val Glu Gly Leu Cys Glu Gly Ile Gly Ala Gly Leu Val Asp
             200                 205                 210

Val Ala Ile Trp Val Gly Thr Cys Ser Asp Tyr Pro Lys Gly Asp
             215                 220                 225

Ala Ser Thr Gly Trp Asn Ser Val Ser Arg Ile Ile Ile Glu Glu
             230                 235                 240

Leu Pro Lys


<210> 353
<211> 480
<212> DNA
<213> Homo sapiens

<400> 353
 gttaaccagc gcagtcctcc gtgcgtcccg cccgccgctg ccctcactcc 50

 cggccaggat ggcatcctgt ctggccctgc gcatggcgct gctgctggtc 100
```

340

tccgggggttc tggcccctgc ggtgctcaca gacgatgttc cacaggagcc 150

cgtgcccacg ctgtggaacg agccggccga gctgccgtcg ggagaaggcc 200

ccgtggagag caccagcccc ggccgggagc ccgtggacac cggtcccca 250

gcccccaccg tcgcgccagg acccgaggac agcaccgcgc aggagcggct 300

ggaccagggc ggcgggtcgc tggggcccgg cgctatcgcg gccatcgtga 350

tcgccgccct gctggccacc tgcgtggtgc tggcgctcgt ggtcgtcgcg 400

ctgagaaagt tttctgcctc ctgaagcgaa taaaggggcc gcgcccggcc 450

gcggcgcgac tcggcaaaaa aaaaaaaaaa 480

<210> 354
<211> 121
<212> PRT
<213> Homo sapiens

<400> 354
```
Met Ala Ser Cys Leu Ala Leu Arg Met Ala Leu Leu Leu Val Ser
 1               5                  10                  15

Gly Val Leu Ala Pro Ala Val Leu Thr Asp Asp Val Pro Gln Glu
                20                  25                  30

Pro Val Pro Thr Leu Trp Asn Glu Pro Ala Glu Leu Pro Ser Gly
                35                  40                  45

Glu Gly Pro Val Glu Ser Thr Ser Pro Gly Arg Glu Pro Val Asp
                50                  55                  60

Thr Gly Pro Pro Ala Pro Thr Val Ala Pro Gly Pro Glu Asp Ser
                65                  70                  75

Thr Ala Gln Glu Arg Leu Asp Gln Gly Gly Gly Ser Leu Gly Pro
                80                  85                  90

Gly Ala Ile Ala Ala Ile Val Ile Ala Ala Leu Leu Ala Thr Cys
                95                  100                 105

Val Val Leu Ala Leu Val Val Val Ala Leu Arg Lys Phe Ser Ala
                110                 115                 120

Ser
```

<210> 355
<211> 2134
<212> DNA
<213> Homo sapiens

<400> 355
ggccgttggt tggtgcgcgg ctgaagggtg tggcgcgagc agcgtcgttg 50

gttggccggc ggcgggccgg gacgggcatg gccctgctgc tgtgcctggt 100

341

```
gtgcctgacg gcggcgctgg cccacggctg tctgcactgc cacagcaact 150

tctccaagaa gttctccttc taccgccacc atgtgaactt caagtcctgg 200

tgggtgggcg acatccccgt gtcaggggcg ctgctcaccg actggagcga 250

cgacacgatg aaggagctgc acctggccat ccccgccaag atcacccggg 300

agaagctgga ccaagtggcg acagcagtgt accagatgat ggatcagctg 350

taccagggga agatgtactt ccccgggtat ttccccaacg agctgcgaaa 400

catcttccgg gagcaggtgc acctcatcca gaacgccatc atcgaaaggc 450

acctggcacc aggcagctgg ggaggagggc agctctccag ggagggaccc 500

agcctagcac ctgaaggatc aatgccatca ccccgcgggg acctccccta 550

agtagccccc agaggcgctg ggagtgttgc caccgccctc ccctgaagtt 600

tgctccatct cacgctgggg gtcaacctgg ggaccccttc cctccgggcc 650

atggacacac atacatgaaa accaggccgc atcgactgtc agcaccgctg 700

tggcatcttc cagtacgaga ccatctcctg caacaactgc acagactcgc 750

acgtcgcctg ctttggctat aactgcgagt agggctcagg catcacaccc 800

acccgtgcca gggccctact gtccctgggg tcccaggctc tccttggagg 850

gggctccccg ccttccacct ggctgtcatc gggtagggcg gggccgtggg 900

ttcaggggcg caccacttcc aagcctgtgt cccacaggtc ctcggcgcag 950

tggaagtcag ctgtccaggg cctcctgaac tacataaata actggcacaa 1000

gtaagtcccc tcctcaaacc aacacaggca gtgtgtgtat gtgagcacct 1050

cgtgggtgag tatgtgtggg gcacaggctg gctccctcag ctcccacgtc 1100

ctagaggggc tcccgaggag gtggaacctc aacccagctc tgcgcaggag 1150

gcggctgcag tccttttctc cctcaaaggt ctccgaccct cagctggagg 1200

cgggcatctt tcctaaaggg tccccatagg gtctggttcc accccatccc 1250

aggtctgtgg tcagagcctg ggagggttcc ctacgatggt taggggtgcc 1300

ccatggaggg gctgactgcc ccacattgcc tttcagacag gacacgagca 1350

tgaggtaagg ccgccctgac ctggacttca gggggagggg gtaaagggag 1400

agaggagggg ggctaggggg tcctctagat cagtggggc actgcaggtg 1450

gggctctccc tatacctggg acacctgctg gatgtcacct ctgcaaccac 1500

acccatgtgg tggtttcatg aacagaccac gctcctctgc cttctcctgg 1550
```

342

```
cctgggacac acagagccac cccggccttg tgagtgaccc agagaaggga 1600

ggcctcggga aagggggtgc tcgtaagcca acaccagcgt gccgcggcct 1650

gcacacccctt cggacatccc aggcacgagg gtgtcgtgga tgtggccaca 1700

cataggacca cacgtcccag ctgggaggag aggcctgggg ccccaggga 1750

gggaggcagg gggtggggga catggagagc tgaggcagcc tcgtctcccc 1800

gcagcctggt atcgccagcc ttaaggtgtc tggagcccccc acacttggcc 1850

aacctgacct tggaagatgc tgctgagtgt ctcaagcagc actgacagca 1900

gctgggcctg ccccagggca acgtgggggc ggagactcag ctggacagcc 1950

cctgcctgtc actctggagc tgggctgctg ctgcctcagg acccccctctc 2000

cgaccccgga cagagctgag ctggccaggg ccaggagggc gggaggagg 2050

gaatgggggt gggctgtgcg cagcatcagc gcctgggcag gtccgcagag 2100

ctgcgggatg tgattaaagt ccctgatgtt tctc 2134
```

<210> 356
<211> 157
<212> PRT
<213> Homo sapiens

<400> 356
```
Met Ala Leu Leu Leu Cys Leu Val Cys Leu Thr Ala Ala Leu Ala
 1               5                  10                  15

His Gly Cys Leu His Cys His Ser Asn Phe Ser Lys Lys Phe Ser
                20                  25                  30

Phe Tyr Arg His His Val Asn Phe Lys Ser Trp Trp Val Gly Asp
                35                  40                  45

Ile Pro Val Ser Gly Ala Leu Leu Thr Asp Trp Ser Asp Asp Thr
                50                  55                  60

Met Lys Glu Leu His Leu Ala Ile Pro Ala Lys Ile Thr Arg Glu
                65                  70                  75

Lys Leu Asp Gln Val Ala Thr Ala Val Tyr Gln Met Met Asp Gln
                80                  85                  90

Leu Tyr Gln Gly Lys Met Tyr Phe Pro Gly Tyr Phe Pro Asn Glu
                95                  100                 105

Leu Arg Asn Ile Phe Arg Glu Gln Val His Leu Ile Gln Asn Ala
                110                 115                 120

Ile Ile Glu Arg His Leu Ala Pro Gly Ser Trp Gly Gly Gly Gln
                125                 130                 135

Leu Ser Arg Glu Gly Pro Ser Leu Ala Pro Glu Gly Ser Met Pro
```

Ser Pro Arg Gly Asp Leu Pro
                    155

<210> 357
<211> 1536
<212> DNA
<213> Homo sapiens

<400> 357
agcaggagca ggagagggac aatggaagct gccccgtcca ggttcatgtt 50

cctcttattt ctcctcacgt gtgagctggc tgcagaagtt gctgcagaag 100

ttgagaaatc ctcagatggt cctggtgctg cccaggaacc cacgtggctc 150

acagatgtcc cagctgccat ggaattcatt gctgccactg aggtggctgt 200

cataggcttc ttccaggatt tagaaatacc agcagtgccc atactccata 250

gcatggtgca aaaattccca ggcgtgtcat ttgggatcag cactgattct 300

gaggttctga cacactacaa catcactggg aacaccatct gcctctttcg 350

cctggtagac aatgaacaac tgaatttaga ggacgaagac attgaaagca 400

ttgatgccac caaattgagc cgtttcattg agatcaacag cctccacatg 450

gtgacagagt acaaccctgt gactgtgatt gggttattca acagcgtaat 500

tcagattcat ctcctcctga taatgaacaa ggcctcccca gagtatgaag 550

agaacatgca cagataccag aaggcagcca agctcttcca ggggaagatt 600

ctctttattc tggtggacag tggtatgaaa gaaaatggga aggtgatatc 650

attttttcaaa ctaaaggagt ctcaactgcc agctttggca atttaccaga 700

ctctagatga cgagtgggat acactgccca gcagaagt ttccgtagag 750

catgtgcaaa acttttgtga tggattccta agtggaaaat tgttgaaaga 800

aaatcgtgaa tcagaaggaa agactccaaa ggtggaactc tgacttctcc 850

ttggaactac atatggccaa gtatctactt tatgcaaagt aaaaaggcac 900

aactcaaatc tcagagacac taaacaacag gatcactagg cctgccaacc 950

acacacacac gcacgtgcac acacgcacgc acgcgtgcac acacacgc 1000

gcacacacac acacacacag agcttcattt cctgtcttaa aatctcgttt 1050

tctcttcttc cttcttttaa atttcatatc ctcactccct atccaatttc 1100

cttcttatcg tgcattcata ctctgtaagc ccatctgtaa cacacctaga 1150

tcaaggcttt aagagactca ctgtgatgcc tctatgaaag agaggcattc 1200

```
ctagagaaag attgttccaa tttgtcattt aatatcaagt ttgtatactg 1250

cacatgactt acacacaaca tagttcctgc tcttttaagg ttacctaagg 1300

gttgaaactc taccttcttt cataagcaca tgtccgtctc tgactcagga 1350

tcaaaaacca aaggatggtt ttaaacacct ttgtgaaatt gtcttttttgc 1400

cagaagttaa aggctgtctc caagtccctg aactcagcag aaatagacca 1450

tgtgaaaact ccatgcttgg ttagcatctc caactcccta tgtaaatcaa 1500

caacctgcat aataaataaa aggcaatcat gttata 1536
```

<210> 358
<211> 273
<212> PRT
<213> Homo sapiens

<400> 358

```
Met Glu Ala Ala Pro Ser Arg Phe Met Phe Leu Leu Phe Leu Leu
 1               5                  10                  15

Thr Cys Glu Leu Ala Ala Glu Val Ala Ala Glu Val Glu Lys Ser
            20                  25                  30

Ser Asp Gly Pro Gly Ala Ala Gln Glu Pro Thr Trp Leu Thr Asp
            35                  40                  45

Val Pro Ala Ala Met Glu Phe Ile Ala Ala Thr Glu Val Ala Val
            50                  55                  60

Ile Gly Phe Phe Gln Asp Leu Glu Ile Pro Ala Val Pro Ile Leu
            65                  70                  75

His Ser Met Val Gln Lys Phe Pro Gly Val Ser Phe Gly Ile Ser
            80                  85                  90

Thr Asp Ser Glu Val Leu Thr His Tyr Asn Ile Thr Gly Asn Thr
            95                  100                 105

Ile Cys Leu Phe Arg Leu Val Asp Asn Glu Gln Leu Asn Leu Glu
            110                 115                 120

Asp Glu Asp Ile Glu Ser Ile Asp Ala Thr Lys Leu Ser Arg Phe
            125                 130                 135

Ile Glu Ile Asn Ser Leu His Met Val Thr Glu Tyr Asn Pro Val
            140                 145                 150

Thr Val Ile Gly Leu Phe Asn Ser Val Ile Gln Ile His Leu Leu
            155                 160                 165

Leu Ile Met Asn Lys Ala Ser Pro Glu Tyr Glu Glu Asn Met His
            170                 175                 180

Arg Tyr Gln Lys Ala Ala Lys Leu Phe Gln Gly Lys Ile Leu Phe
            185                 190                 195
```

345

```
Ile Leu Val Asp Ser Gly Met Lys Glu Asn Gly Lys Val Ile Ser
            200             205             210

Phe Phe Lys Leu Lys Glu Ser Gln Leu Pro Ala Leu Ala Ile Tyr
            215             220             225

Gln Thr Leu Asp Asp Glu Trp Asp Thr Leu Pro Thr Ala Glu Val
            230             235             240

Ser Val Glu His Val Gln Asn Phe Cys Asp Gly Phe Leu Ser Gly
            245             250             255

Lys Leu Leu Lys Glu Asn Arg Glu Ser Glu Gly Lys Thr Pro Lys
            260             265             270

Val Glu Leu
```

<210> 359
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 359
 ccagcagtgc ccatactcca tagc 24

<210> 360
<211> 20
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-20
<223> Synthetic construct.

<400> 360
 tgacgagtgg gatacactgc 20

<210> 361
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 361
 gctctacgga aacttctgct gtgg 24

<210> 362

<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 362
 attcccaggc gtgtcatttg ggatcagcac tgattctgag gttctgacac 50

<210> 363
<211> 1777
<212> DNA
<213> Homo sapiens

<400> 363
 ggagagccgc ggctgggacc ggagtgggga gcgcggcgtg gaggtgccac 50

 ccggcgcggg tggcggagag atcagaagcc tcttccccaa gccgagccaa 100

 cctcagcggg gacccgggct cagggacgcg gcggcggcgg cggcgactgc 150

 agtggctgga cgatggcagc gtccgccgga gccggggcgg tgattgcagc 200

 cccagacagc cggcgctggc tgtggtcggt gctggcggcg gcgcttgggc 250

 tcttgacagc tggagtatca gccttggaag tatatacgcc aaaagaaatc 300

 ttcgtggcaa atggtacaca agggaagctg acctgcaagt tcaagtctac 350

 tagtacgact ggcgggttga cctcagtctc ctggagcttc cagccagagg 400

 gggccgacac tactgtgtcg tttttccact actcccaagg gcaagtgtac 450

 cttgggaatt atccaccatt taaagacaga atcagctggg ctggagacct 500

 tgacaagaaa gatgcatcaa tcaacataga aaatatgcag tttatacaca 550

 atggcaccta tatctgtgat gtcaaaaacc ctcctgacat cgttgtccag 600

 cctggacaca ttaggctcta tgtcgtagaa aaagagaatt gcctgtgtt 650

 tccagtttgg gtagtggtgg gcatagttac tgctgtggtc ctaggtctca 700

 ctctgctcat cagcatgatt ctggctgtcc tctatagaag gaaaaactct 750

 aaacgggatt acactggctg cagtacatca gagagtttgt caccagttaa 800

 gcaggctcct cggaagtccc cctccgacac tgagggtctt gtaaagagtc 850

 tgccttctgg atctcaccag ggcccagtca tatatgcaca gttagaccac 900

 tccggcggac atcacagtga caagattaac aagtcagagt ctgtggtgta 950

 tgcggatatc cgaaagaatt aagagaatac ctagaacata tcctcagcaa 1000

347

```
gaaacaaaac caaactggac tctcgtgcag aaaatgtagc ccattaccac 1050

atgtagcctt ggagacccag gcaaggacaa gtacacgtgt actcacagag 1100

ggagagaaag atgtgtacaa aggatatgta taaatattct atttagtcat 1150

cctgatatga ggagccagtg ttgcatgatg aaaagatggt atgattctac 1200

atatgtaccc attgtcttgc tgtttttgta ctttcttttc aggtcattta 1250

caattgggag atttcagaaa cattcctttc accatcattt agaaatggtt 1300

tgccttaatg gagacaatag cagatcctgt agtatttcca gtagacatgg 1350

ccttttaatc taagggctta agactgatta gtcttagcat ttactgtagt 1400

tggaggatgg agatgctatg atggaagcat acccagggtg gcctttagca 1450

cagtatcagt accatttatt tgtctgccgc ttttaaaaaa tacccattgg 1500

ctatgccact tgaaaacaat ttgagaagtt tttttgaagt ttttctcact 1550

aaaatatggg gcaattgtta gccttacatg ttgtgtagac ttactttaag 1600

tttgcaccct tgaaatgtgt catatcaatt tctggattca taatagcaag 1650

attagcaaag gataaatgcc gaaggtcact tcattctgga cacagttgga 1700

tcaatactga ttaagtagaa aatccaagct ttgcttgaga acttttgtaa 1750

cgtggagagt aaaaagtatc ggtttta 1777
```

<210> 364
<211> 269
<212> PRT
<213> Homo sapiens

<400> 364

```
Met Ala Ala Ser Ala Gly Ala Gly Ala Val Ile Ala Ala Pro Asp
1               5                   10                  15

Ser Arg Arg Trp Leu Trp Ser Val Leu Ala Ala Ala Leu Gly Leu
                20                  25                  30

Leu Thr Ala Gly Val Ser Ala Leu Glu Val Tyr Thr Pro Lys Glu
                35                  40                  45

Ile Phe Val Ala Asn Gly Thr Gln Gly Lys Leu Thr Cys Lys Phe
                50                  55                  60

Lys Ser Thr Ser Thr Thr Gly Gly Leu Thr Ser Val Ser Trp Ser
                65                  70                  75

Phe Gln Pro Glu Gly Ala Asp Thr Thr Val Ser Phe Phe His Tyr
                80                  85                  90

Ser Gln Gly Gln Val Tyr Leu Gly Asn Tyr Pro Pro Phe Lys Asp
                95                  100                 105
```

348

```
Arg Ile Ser Trp Ala Gly Asp Leu Asp Lys Lys Asp Ala Ser Ile
            110             115             120
Asn Ile Glu Asn Met Gln Phe Ile His Asn Gly Thr Tyr Ile Cys
            125             130             135
Asp Val Lys Asn Pro Pro Asp Ile Val Val Gln Pro Gly His Ile
            140             145             150
Arg Leu Tyr Val Val Glu Lys Glu Asn Leu Pro Val Phe Pro Val
            155             160             165
Trp Val Val Val Gly Ile Val Thr Ala Val Val Leu Gly Leu Thr
            170             175             180
Leu Leu Ile Ser Met Ile Leu Ala Val Leu Tyr Arg Arg Lys Asn
            185             190             195
Ser Lys Arg Asp Tyr Thr Gly Cys Ser Thr Ser Glu Ser Leu Ser
            200             205             210
Pro Val Lys Gln Ala Pro Arg Lys Ser Pro Ser Asp Thr Glu Gly
            215             220             225
Leu Val Lys Ser Leu Pro Ser Gly Ser His Gln Gly Pro Val Ile
            230             235             240
Tyr Ala Gln Leu Asp His Ser Gly Gly His His Ser Asp Lys Ile
            245             250             255
Asn Lys Ser Glu Ser Val Val Tyr Ala Asp Ile Arg Lys Asn
            260             265
```

<210> 365
<211> 1321
<212> DNA
<213> Homo sapiens

<400> 365
```
gccggctgtg cagagacgcc atgtaccggc tcctgtcagc agtgactgcc  50

cgggctgccg cccccggggg cttggcctca agctgcggac gacgcggggt 100

ccatcagcgc gccgggctgc cgcctctcgg ccacggctgg gtcgggggcc 150

tcgggctggg gctggggctg gcgctcgggg tgaagctggc aggtgggctg 200

aggggcgcgg ccccggcgca gtcccccgcg gcccccgacc ctgaggcgtc 250

gcctctggcc gagccgccac aggagcagtc cctcgccccg tggtctccgc 300

agaccccggc gccgccctgc tccaggtgct tcgccagagc catcgagagc 350

agccgcgacc tgctgcacag gatcaaggat gaggtgggcg caccgggcat 400

agtggttgga gtttctgtag atggaaaaga agtctggtca gaaggtttag 450

gttatgctga tgttgagaac cgtgtaccat gtaaaccaga gacagttatg 500
```

```
cgaattgcta gcatcagcaa aagtctcacc atggttgctc ttgccaaatt 550

gtgggaagca gggaaactgg atcttgatat tccagtacaa cattatgttc 600

ccgaattccc agaaaaagaa tatgaaggtg aaaaggtttc tgtcacaaca 650

agattactga tttcccattt aagtggaatt cgtcattatg aaaaggacat 700

aaaaaaggtg aaagaagaga agcttataa agccttgaag atgatgaaag 750

agaatgttgc atttgagcaa gaaaaagaag gcaaaagtaa tgaaaagaat 800

gattttacta aatttaaaac agagcaggag aatgaagcca atgccggaa 850

ttcaaaacct ggcaagaaaa agaatgattt tgaacaaggc gaattatatt 900

tgagagaaaa gtttgaaaat tcaattgaat ccctaagatt atttaaaaat 950

gatcctttgt tcttcaaacc tggtagtcag ttttttgtatt caacttttgg 1000

ctataccccta ctggcagcca tagtagagag agcttcagga tgtaaatatt 1050

tggactatat gcagaaaata ttccatgact tggatatgct gacgactgtg 1100

caggaagaaa acgagccagt gatttacaat agagcaaggt aaatgaatac 1150

cttctgctgt gtctagctat atcgcatctt aacactattt tattaattaa 1200

aagtcaaatt ttctttgttt ccattccaaa atcaacctgc cacattttgg 1250

gagctttct acatgtctgt tttctcatct gtaaagtgaa ggaagtaaaa 1300

catgtttata aagtaaaaaa a 1321
```

<210> 366
<211> 373
<212> PRT
<213> Homo sapiens

<400> 366

```
Met Tyr Arg Leu Leu Ser Ala Val Thr Ala Arg Ala Ala Ala Pro
1               5                  10                  15

Gly Gly Leu Ala Ser Ser Cys Gly Arg Arg Gly Val His Gln Arg
            20                  25                  30

Ala Gly Leu Pro Pro Leu Gly His Gly Trp Val Gly Gly Leu Gly
            35                  40                  45

Leu Gly Leu Gly Leu Ala Leu Gly Val Lys Leu Ala Gly Gly Leu
            50                  55                  60

Arg Gly Ala Ala Pro Ala Gln Ser Pro Ala Ala Pro Asp Pro Glu
            65                  70                  75

Ala Ser Pro Leu Ala Glu Pro Pro Gln Glu Gln Ser Leu Ala Pro
            80                  85                  90
```

350
```

```
Trp Ser Pro Gln Thr Pro Ala Pro Pro Cys Ser Arg Cys Phe Ala
                 95              100                     105

Arg Ala Ile Glu Ser Ser Arg Asp Leu Leu His Arg Ile Lys Asp
                110              115                     120

Glu Val Gly Ala Pro Gly Ile Val Val Gly Val Ser Val Asp Gly
                125              130                     135

Lys Glu Val Trp Ser Glu Gly Leu Gly Tyr Ala Asp Val Glu Asn
                140              145                     150

Arg Val Pro Cys Lys Pro Glu Thr Val Met Arg Ile Ala Ser Ile
                155              160                     165

Ser Lys Ser Leu Thr Met Val Ala Leu Ala Lys Leu Trp Glu Ala
                170              175                     180

Gly Lys Leu Asp Leu Asp Ile Pro Val Gln His Tyr Val Pro Glu
                185              190                     195

Phe Pro Glu Lys Glu Tyr Glu Gly Glu Lys Val Ser Val Thr Thr
                200              205                     210

Arg Leu Leu Ile Ser His Leu Ser Gly Ile Arg His Tyr Glu Lys
                215              220                     225

Asp Ile Lys Lys Val Lys Glu Glu Lys Ala Tyr Lys Ala Leu Lys
                230              235                     240

Met Met Lys Glu Asn Val Ala Phe Glu Gln Glu Lys Glu Gly Lys
                245              250                     255

Ser Asn Glu Lys Asn Asp Phe Thr Lys Phe Lys Thr Glu Gln Glu
                260              265                     270

Asn Glu Ala Lys Cys Arg Asn Ser Lys Pro Gly Lys Lys Lys Asn
                275              280                     285

Asp Phe Glu Gln Gly Glu Leu Tyr Leu Arg Glu Lys Phe Glu Asn
                290              295                     300

Ser Ile Glu Ser Leu Arg Leu Phe Lys Asn Asp Pro Leu Phe Phe
                305              310                     315

Lys Pro Gly Ser Gln Phe Leu Tyr Ser Thr Phe Gly Tyr Thr Leu
                320              325                     330

Leu Ala Ala Ile Val Glu Arg Ala Ser Gly Cys Lys Tyr Leu Asp
                335              340                     345

Tyr Met Gln Lys Ile Phe His Asp Leu Asp Met Leu Thr Thr Val
                350              355                     360

Gln Glu Glu Asn Glu Pro Val Ile Tyr Asn Arg Ala Arg
                365              370

<210> 367
```

```
<211> 30
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-30
<223> Synthetic construct.

<400> 367
 tggaaaagaa gtctggtcag aaggtttagg 30

<210> 368
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-25
<223> Synthetic construct.

<400> 368
 catttggctt cattctcctg ctctg 25

<210> 369
<211> 28
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-28
<223> Synthetic construct.

<400> 369
 aaaacctcag aacaactcat tttgcacc 28

<210> 370
<211> 41
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-41
<223> Synthetic construct.

<400> 370
 gtctcaccat ggttgctctt gccaaattgt gggaagcagg g 41

<210> 371
<211> 1150
<212> DNA
<213> Homo sapiens

<400> 371
 gtgacactat agaagagcta tgacgtcgca tgcacgcgta cgtaagctcg 50
```

gaattcggct cgaggctggt gggaagaagc cgagatggcg gcagccagcg 100

ctggggcaac ccggctgctc ctgctcttgc tgatggcggt agcagcgccc 150

agtcgagccc ggggcagcgg ctgccgggcc gggactggtg cgcgaggggc 200

tggggcggaa ggtcgagagg gcgaggcctg tggcacggtg gggctgctgc 250

tggagcactc atttgagatc gatgacagtg ccaacttccg gaagcggggc 300

tcactgctct ggaaccagca ggatggtacc ttgtccctgt cacagcggca 350

gctcagcgag gaggagcggg gccgactccg ggatgtggca gccctgaatg 400

gcctgtaccg ggtccggatc ccaaggcgac ccggggccct ggatggcctg 450

gaagctggtg gctatgtctc ctcctttgtc cctgcgtgct ccctggtgga 500

gtcgcacctg tcggaccagc tgaccctgca cgtggatgtg gccggcaacg 550

tggtgggcgt gtcggtggtg acgcaccccg ggggctgccg gggccatgag 600

gtggaggacg tggacctgga gctgttcaac acctcggtgc agctgcagcc 650

gcccaccaca gccccaggcc ctgagacggc ggccttcatt gagcgcctgg 700

agatggaaca ggcccagaag gccaagaacc cccaggagca gaagtccttc 750

ttcgccaaat actggatgta catcattccc gtcgtcctgt tcctcatgat 800

gtcaggagcg ccagacaccg ggggccaggg tggggggtggg ggtggggggtg 850

gtggtggggg tagtggcctt tgctgtgtgc caccctccct gtaagtctat 900

ttaaaaacat cgacgataca ttgaaatgtg tgaacgtttt gaaaagctac 950

agcttccagc agccaaaagc aactgttgtt ttggcaagac ggtcctgatg 1000

tacaagcttg attgaaattc actgctcact tgatacgtta ttcagaaacc 1050

caaggaatgg ctgtccccat cctcatgtgg ctgtgtggag ctcagctgtg 1100

ttgtgtggca gtttattaaa ctgtccccca gatcgacacg caaaaaaaaa 1150

<210> 372
<211> 269
<212> PRT
<213> Homo sapiens

<400> 372
Met Ala Ala Ala Ser Ala Gly Ala Thr Arg Leu Leu Leu Leu
  1   5   10   15

Leu Met Ala Val Ala Ala Pro Ser Arg Ala Arg Gly Ser Gly Cys
                 20   25   30

Arg Ala Gly Thr Gly Ala Arg Gly Ala Gly Ala Glu Gly Arg Glu
                 35   40   45

353

```
Gly Glu Ala Cys Gly Thr Val Gly Leu Leu Leu Glu His Ser Phe
              50                  55                  60

Glu Ile Asp Asp Ser Ala Asn Phe Arg Lys Arg Gly Ser Leu Leu
              65                  70                  75

Trp Asn Gln Gln Asp Gly Thr Leu Ser Leu Ser Gln Arg Gln Leu
              80                  85                  90

Ser Glu Glu Glu Arg Gly Arg Leu Arg Asp Val Ala Ala Leu Asn
              95                 100                 105

Gly Leu Tyr Arg Val Arg Ile Pro Arg Arg Pro Gly Ala Leu Asp
             110                 115                 120

Gly Leu Glu Ala Gly Gly Tyr Val Ser Ser Phe Val Pro Ala Cys
             125                 130                 135

Ser Leu Val Glu Ser His Leu Ser Asp Gln Leu Thr Leu His Val
             140                 145                 150

Asp Val Ala Gly Asn Val Val Gly Val Ser Val Val Thr His Pro
             155                 160                 165

Gly Gly Cys Arg Gly His Glu Val Glu Asp Val Asp Leu Glu Leu
             170                 175                 180

Phe Asn Thr Ser Val Gln Leu Gln Pro Pro Thr Thr Ala Pro Gly
             185                 190                 195

Pro Glu Thr Ala Ala Phe Ile Glu Arg Leu Glu Met Glu Gln Ala
             200                 205                 210

Gln Lys Ala Lys Asn Pro Gln Glu Gln Lys Ser Phe Phe Ala Lys
             215                 220                 225

Tyr Trp Met Tyr Ile Ile Pro Val Val Leu Phe Leu Met Met Ser
             230                 235                 240

Gly Ala Pro Asp Thr Gly Gly Gln Gly Gly Gly Gly Gly Gly Gly
             245                 250                 255

Gly Gly Gly Gly Ser Gly Leu Cys Cys Val Pro Pro Ser Leu
             260                 265
```

<210> 373
<211> 1706
<212> DNA
<213> Homo sapiens

<400> 373
```
ggagcgctgc tggaacccga gccggagccg agccacagc ggggagggtg  50

gcctggcggc ctggagccgg acgtgtccgg ggcgtccccg cagaccgggg 100

cagcaggtcg tccggggggcc caccatgctg gtgactgcct accttgcttt 150

tgtaggcctc ctggcctcct gcctggggct ggaactgtca agatgccggg 200
```

354

ctaaacccc tggaagggcc tgcagcaatc cctccttcct tcggtttcaa 250

ctggacttct atcaggtcta cttcctggcc ctggcagctg attggcttca 300

ggcccctac ctctataaac tctaccagca ttactacttc ctggaaggtc 350

aaattgccat cctctatgtc tgtggccttg cctctacagt cctctttggc 400

ctagtggcct cctcccttgt ggattggctg ggtcgcaaga attcttgtgt 450

cctcttctcc ctgacttact cactatgctg cttaaccaaa ctctctcaag 500

actactttgt gctgctagtg gggcgagcac ttggtgggct gtccacagcc 550

ctgctcttct cagccttcga ggcctggtat atccatgagc acgtggaacg 600

gcatgacttc cctgctgagt ggatcccagc tacctttgct cgagctgcct 650

tctggaacca tgtgctggct gtagtggcag gtgtggcagc tgaggctgta 700

gccagctgga tagggctggg gcctgtagcg ccctttgtgg ctgccatccc 750

tctcctggct ctggcagggg ccttggccct tcgaaactgg ggggagaact 800

atgaccggca gcgtgccttc tcaaggacct gtgctggagg cctgcgctgc 850

ctcctgtcgg accgccgcgt gctgctgctg ggcaccatac aagctctatt 900

tgagagtgtc atcttcatct ttgtcttcct ctggacacct gtgctggacc 950

cacacggggc ccctctgggc attatcttct ccagcttcat ggcagccagc 1000

ctgcttggct cttccctgta ccgtatcgcc acctccaaga ggtaccacct 1050

tcagcccatg cacctgctgt cccttgctgt gctcatcgtc gtcttctctc 1100

tcttcatgtt gactttctct accagcccag gccaggagag tccggtggag 1150

tccttcatag cctttctact tattgagttg gcttgtggat tatactttcc 1200

cagcatgagc ttcctacgga gaaaggtgat ccctgagaca gagcaggctg 1250

gtgtactcaa ctggttccgg gtacctctgc actcactggc ttgcctaggg 1300

ctccttgtcc tccatgacag tgatcgaaaa acaggcactc ggaatatgtt 1350

cagcatttgc tctgctgtca tggtgatggc tctgctggca gtggtgggac 1400

tcttcaccgt ggtaaggcat gatgctgagc tgcgggtacc ttcacctact 1450

gaggagccct atgcccctga ctgtaaccc cactccagga caagatagct 1500

gggacagact cttgaattcc agctatccgg gattgtacag atctctctgt 1550

gactgacttt gtgactgtcc tgtggtttct cctgccattg ctttgtgttt 1600

gggaggacat gatgggggtg atggactgga agaaggtgc caaaagttcc 1650

355

ctctgtgtta ctcccattta gaaaataaac acttttaaat gatcaaaaaa 1700

aaaaaa 1706

<210> 374
<211> 450
<212> PRT
<213> Homo sapiens

<400> 374
Met Leu Val Thr Ala Tyr Leu Ala Phe Val Gly Leu Leu Ala Ser
1   5   10   15

Cys Leu Gly Leu Glu Leu Ser Arg Cys Arg Ala Lys Pro Pro Gly
                20   25   30

Arg Ala Cys Ser Asn Pro Ser Phe Leu Arg Phe Gln Leu Asp Phe
                35   40   45

Tyr Gln Val Tyr Phe Leu Ala Leu Ala Ala Asp Trp Leu Gln Ala
                50   55   60

Pro Tyr Leu Tyr Lys Leu Tyr Gln His Tyr Tyr Phe Leu Glu Gly
                65   70   75

Gln Ile Ala Ile Leu Tyr Val Cys Gly Leu Ala Ser Thr Val Leu
                80   85   90

Phe Gly Leu Val Ala Ser Ser Leu Val Asp Trp Leu Gly Arg Lys
                95   100   105

Asn Ser Cys Val Leu Phe Ser Leu Thr Tyr Ser Leu Cys Cys Leu
                110   115   120

Thr Lys Leu Ser Gln Asp Tyr Phe Val Leu Leu Val Gly Arg Ala
                125   130   135

Leu Gly Gly Leu Ser Thr Ala Leu Leu Phe Ser Ala Phe Glu Ala
                140   145   150

Trp Tyr Ile His Glu His Val Glu Arg His Asp Phe Pro Ala Glu
                155   160   165

Trp Ile Pro Ala Thr Phe Ala Arg Ala Ala Phe Trp Asn His Val
                170   175   180

Leu Ala Val Val Ala Gly Val Ala Ala Glu Ala Val Ala Ser Trp
                185   190   195

Ile Gly Leu Gly Pro Val Ala Pro Phe Val Ala Ala Ile Pro Leu
                200   205   210

Leu Ala Leu Ala Gly Ala Leu Ala Leu Arg Asn Trp Gly Glu Asn
                215   220   225

Tyr Asp Arg Gln Arg Ala Phe Ser Arg Thr Cys Ala Gly Gly Leu
                230   235   240

356

```
Arg Cys Leu Leu Ser Asp Arg Arg Val Leu Leu Leu Gly Thr Ile
                245             250             255

Gln Ala Leu Phe Glu Ser Val Ile Phe Ile Phe Val Phe Leu Trp
                260             265             270

Thr Pro Val Leu Asp Pro His Gly Ala Pro Leu Gly Ile Ile Phe
                275             280             285

Ser Ser Phe Met Ala Ala Ser Leu Leu Gly Ser Ser Leu Tyr Arg
                290             295             300

Ile Ala Thr Ser Lys Arg Tyr His Leu Gln Pro Met His Leu Leu
                305             310             315

Ser Leu Ala Val Leu Ile Val Val Phe Ser Leu Phe Met Leu Thr
                320             325             330

Phe Ser Thr Ser Pro Gly Gln Glu Ser Pro Val Glu Ser Phe Ile
                335             340             345

Ala Phe Leu Leu Ile Glu Leu Ala Cys Gly Leu Tyr Phe Pro Ser
                350             355             360

Met Ser Phe Leu Arg Arg Lys Val Ile Pro Glu Thr Glu Gln Ala
                365             370             375

Gly Val Leu Asn Trp Phe Arg Val Pro Leu His Ser Leu Ala Cys
                380             385             390

Leu Gly Leu Leu Val Leu His Asp Ser Asp Arg Lys Thr Gly Thr
                395             400             405

Arg Asn Met Phe Ser Ile Cys Ser Ala Val Met Val Met Ala Leu
                410             415             420

Leu Ala Val Val Gly Leu Phe Thr Val Val Arg His Asp Ala Glu
                425             430             435

Leu Arg Val Pro Ser Pro Thr Glu Glu Pro Tyr Ala Pro Glu Leu
                440             445             450
```

<210> 375
<211> 1098
<212> DNA
<213> Artificial

<400> 375

```
gcgacgcgcg gcggggcggc gagaggaaac gcggcgccgg gccgggcccg 50

gccctggaga tggtccccgg cgccgcgggc tggtgttgtc tcgtgctctg 100

gctccccgcg tgcgtcgcgg cccacggctt ccgtatccat gattatttgt 150

actttcaagt gctgagtcct ggggacattc gatacatctt cacagccaca 200

cctgccaagg actttggtgg tatctttcac acaaggtatg agcagattca 250
```

357

```
ccttgtcccc gctgaacctc cagaggcctg cggggaactc agcaacggtt 300

tcttcatcca ggaccagatt gctctggtgg agaggggggg ctgctccttc 350

ctctccaaga ctcgggtggt ccaggagcac ggcgggcggg cggtgatcat 400

ctctgacaac gcagttgaca atgacagctt ctacgtggag atgatccagg 450

acagtaccca gcgcacagct gacatccccg ccctcttcct gctcggccga 500

gacggctaca tgatccgccg ctctctggaa cagcatgggc tgccatgggc 550

catcatttcc atcccagtca atgtcaccag catccccacc tttgagctgc 600

tgcaaccgcc ctggaccttc tggtagaaga gtttgtccca cattccagcc 650

ataagtgact ctgagctggg aaggggaaac ccaggaattt tgctacttgg 700

aatttggaga tagcatctgg ggacaagtgg agccaggtag aggaaaaggg 750

tttgggcgtt gctaggctga aagggaagcc acaccactgg ccttcccttc 800

cccagggccc ccaagggtgt ctcatgctac aagaagaggc aagagacagg 850

ccccagggct tctggctaga acccgaaaca aaaggagctg aaggcaggtg 900

gcctgagagc catctgtgac ctgtcacact cacctggctc cagcctcccc 950

tacccagggt ctctgcacag tgaccttcac agcagttgtt ggagtggttt 1000

aaagagctgg tgtttgggga ctcaataaac cctcactgac tttttagcaa 1050

taaagcttct catcagggtt gcaaaaaaaa aaaaaaaaaa aaaaaaaa 1098

<210> 376
<211> 188
<212> PRT
<213> Homo sapiens

<400> 376
Met Val Pro Gly Ala Ala Gly Trp Cys Cys Leu Val Leu Trp Leu
  1               5                  10                  15

Pro Ala Cys Val Ala Ala His Gly Phe Arg Ile His Asp Tyr Leu
               20                  25                  30

Tyr Phe Gln Val Leu Ser Pro Gly Asp Ile Arg Tyr Ile Phe Thr
               35                  40                  45

Ala Thr Pro Ala Lys Asp Phe Gly Gly Ile Phe His Thr Arg Tyr
               50                  55                  60

Glu Gln Ile His Leu Val Pro Ala Glu Pro Pro Glu Ala Cys Gly
               65                  70                  75

Glu Leu Ser Asn Gly Phe Phe Ile Gln Asp Gln Ile Ala Leu Val
               80                  85                  90
```

358

```
Glu Arg Gly Gly Cys Ser Phe Leu Ser Lys Thr Arg Val Val Gln
              95                  100                 105

Glu His Gly Gly Arg Ala Val Ile Ile Ser Asp Asn Ala Val Asp
              110                 115                 120

Asn Asp Ser Phe Tyr Val Glu Met Ile Gln Asp Ser Thr Gln Arg
              125                 130                 135

Thr Ala Asp Ile Pro Ala Leu Phe Leu Leu Gly Arg Asp Gly Tyr
              140                 145                 150

Met Ile Arg Arg Ser Leu Glu Gln His Gly Leu Pro Trp Ala Ile
              155                 160                 165

Ile Ser Ile Pro Val Asn Val Thr Ser Ile Pro Thr Phe Glu Leu
              170                 175                 180

Leu Gln Pro Pro Trp Thr Phe Trp
              185
```

<210> 377
<211> 496
<212> DNA
<213> Artificial

<220>
<221> unsure
<222> 396
<223> unknown base

<400> 377
```
 tctgcctcca ctgctctgtg ctgggatcat ggaacttgca ctgctgtgtg   50

 ggctggtggt gatggctggt gtgattccaa tccagggcgg gatcctgaac  100

 ctgaacaaga tggtcaagca agtgactggg aaaatgccca tcctctccta  150

 ctggccctac ggctgtcact gcggactagg tggcagaggc caacccaaag  200

 atgccacgga ctggtgctgc cagacccatg actgctgcta tgaccacctg  250

 aagacccagg ggtgcggcat ctacaaggac aacaacaaaa gcagcataca  300

 ttgtatggat ttatctcaac gctattgttt aatggctgtg tttaatgtga  350

 tctatctgga aaatgaggac tccgaataaa aagctattac tawttnaaaa  400

 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa  450

 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa      496
```

<210> 378
<211> 116
<212> PRT
<213> Homo sapiens

<400> 378
```

```
Met Glu Leu Ala Leu Leu Cys Gly Leu Val Val Met Ala Gly Val
 1               5                   10                  15

Ile Pro Ile Gln Gly Gly Ile Leu Asn Leu Asn Lys Met Val Lys
                 20                  25                  30

Gln Val Thr Gly Lys Met Pro Ile Leu Ser Tyr Trp Pro Tyr Gly
                 35                  40                  45

Cys His Cys Gly Leu Gly Gly Arg Gly Gln Pro Lys Asp Ala Thr
                 50                  55                  60

Asp Trp Cys Cys Gln Thr His Asp Cys Cys Tyr Asp His Leu Lys
                 65                  70                  75

Thr Gln Gly Cys Gly Ile Tyr Lys Asp Asn Asn Lys Ser Ser Ile
                 80                  85                  90

His Cys Met Asp Leu Ser Gln Arg Tyr Cys Leu Met Ala Val Phe
                 95                  100                 105

Asn Val Ile Tyr Leu Glu Asn Glu Asp Ser Glu
                 110                 115
```

<210> 379
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 379
 ctgcctccac tgctctgtgc tggg 24

<210> 380
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 380
 cagagcagtg gatgttcccc tggg 24

<210> 381
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45

<223> Synthetic construct.

<400> 381
ctgaacaaga tggtcaagca agtgactggg aaaatgccca tcctc 45

<210> 382
<211> 764
<212> DNA
<213> Homo sapiens

<400> 382
ctcgcttctt ccttctggat gggggcccag ggggcccagg agagtataaa 50

ggcgatgtgg agggtgcccg gcacaaccag acgcccagtc acaggcgaga 100

gccctgggat gcaccggcca gaggccatgc tgctgctgct cacgcttgcc 150

ctcctggggg gccccacctg ggcagggaag atgtatggcc ctggaggagg 200

caagtatttc agcaccactg aagactacga ccatgaaatc acaggctgc 250

gggtgtctgt aggtcttctc ctggtgaaaa gtgtccaggt gaaacttgga 300

gactcctggg acgtgaaact gggagcctta ggtgggaata cccaggaagt 350

caccctgcag ccaggcgaat acatcacaaa agtctttgtc gccttccaag 400

ctttcctccg gggtatggtc atgtacacca gcaaggaccg ctatttctat 450

tttgggaagc ttgatggcca gatctcctct gcctacccca gccaagaggg 500

gcaggtgctg gtgggcatct atggccagta tcaactcctt ggcatcaaga 550

gcattggctt tgaatggaat tatccactag aggagccgac cactgagcca 600

ccagttaatc tcacatactc agcaaactca cccgtgggtc gctagggtgg 650

ggtatggggc catccgagct gaggccatct gtgtggtggt ggctgatggt 700

actggagtaa ctgagtcggg acgctgaatc tgaatccacc aataaataaa 750

gcttctgcag aaaa 764

<210> 383
<211> 178
<212> PRT
<213> Homo sapiens

<400> 383
```
Met His Arg Pro Glu Ala Met Leu Leu Leu Thr Leu Ala Leu
 1               5              10              15

Leu Gly Gly Pro Thr Trp Ala Gly Lys Met Tyr Gly Pro Gly Gly
             20          25              30

Gly Lys Tyr Phe Ser Thr Thr Glu Asp Tyr Asp His Glu Ile Thr
         35              40              45
```

```
Gly Leu Arg Val Ser Val Gly Leu Leu Leu Val Lys Ser Val Gln
            50                  55                  60

Val Lys Leu Gly Asp Ser Trp Asp Val Lys Leu Gly Ala Leu Gly
            65                  70                  75

Gly Asn Thr Gln Glu Val Thr Leu Gln Pro Gly Glu Tyr Ile Thr
            80                  85                  90

Lys Val Phe Val Ala Phe Gln Ala Phe Leu Arg Gly Met Val Met
            95                  100                 105

Tyr Thr Ser Lys Asp Arg Tyr Phe Tyr Phe Gly Lys Leu Asp Gly
            110                 115                 120

Gln Ile Ser Ser Ala Tyr Pro Ser Gln Glu Gly Gln Val Leu Val
            125                 130                 135

Gly Ile Tyr Gly Gln Tyr Gln Leu Leu Gly Ile Lys Ser Ile Gly
            140                 145                 150

Phe Glu Trp Asn Tyr Pro Leu Glu Glu Pro Thr Thr Glu Pro Pro
            155                 160                 165

Val Asn Leu Thr Tyr Ser Ala Asn Ser Pro Val Gly Arg
            170                 175
```

<210> 384
<211> 2379
<212> DNA
<213> Homo sapiens

<400> 384

```
gctgagcgtg tgcgcggtac ggggctctcc tgccttctgg gctccaacgc 50

agctctgtgg ctgaactggg tgctcatcac gggaactgct gggctatgga 100

atacagatgt ggcagctcag gtagccccaa attgcctgga agaatacatc 150

atgttttcg ataagaagaa attgtaggat ccagtttttt ttttaaccgc 200

cccctcccca cccccaaaa aaactgtaaa gatgcaaaaa cgtaatatcc 250

atgaagatcc tattacctag gaagattttg atgttttgct gcgaatgcgg 300

tgttgggatt tatttgttct tggagtgttc tgcgtggctg gcaaagaata 350

atgttccaaa atcggtccat ctcccaaggg gtccaatttt tcttcctggg 400

tgtcagcgag ccctgactca ctacagtgca gctgacaggg ctgtcatgc 450

aactggcccc taagccaaag caaaagacct aaggacgacc tttgaacaat 500

acaaaggatg ggtttcaatg taattaggct actgagcgga tcagctgtag 550

cactggttat agccccccact gtcttactga caatgctttc ttctgccgaa 600

cgaggatgcc ctaagggctg taggtgtgaa ggcaaaatgg tatattgtga 650
```

362

```
atctcagaaa ttacaggaga taccctcaag tatatctgct ggttgcttag 700

gtttgtccct tcgctataac agccttcaaa aacttaagta taatcaattt 750

aaagggctca accagctcac ctggctatac cttgaccata accatatcag 800

caatattgac gaaaatgctt ttaatggaat acgcagactc aaagagctga 850

ttcttagttc caatagaatc tcctattttc ttaacaatac cttcagacct 900

gtgacaaatt tacggaactt ggatctgtcc tataatcagc tgcattctct 950

gggatctgaa cagtttcggg gcttgcggaa gctgctgagt ttacatttac 1000

ggtctaactc cctgagaacc atccctgtgc gaatattcca agactgccgc 1050

aacctggaac ttttggacct gggatataac cggatccgaa gtttagccag 1100

gaatgtcttt gctggcatga tcagactcaa agaacttcac ctggagcaca 1150

atcaattttc caagctcaac ctggcccttt ttccaaggtt ggtcagcctt 1200

cagaaccttt acttgcagtg gaataaaatc agtgtcatag gacagaccat 1250

gtcctggacc tggagctcct tacaaaggct tgatttatca ggcaatgaga 1300

tcgaagcttt cagtggaccc agtgttttcc agtgtgtccc gaatctgcag 1350

cgcctcaacc tggattccaa caagctcaca tttattggtc aagagatttt 1400

ggattcttgg atatccctca atgacatcag tcttgctggg aatatatggg 1450

aatgcagcag aaatatttgc tcccttgtaa actggctgaa aagttttaaa 1500

ggtctaaggg agaatacaat tatctgtgcc agtcccaaag agctgcaagg 1550

agtaaatgtg atcgatgcag tgaagaacta cagcatctgt ggcaaaagta 1600

ctacagagag gtttgatctg gccagggctc tcccaaagcc gacgtttaag 1650

cccaagctcc ccaggccgaa gcatgagagc aaaccccctt tgcccccgac 1700

ggtgggagcc acagagcccg gcccagagac cgatgctgac gccgagcaca 1750

tctctttcca taaaatcatc gcgggcagcg tggcgctttt cctgtccgtg 1800

ctcgtcatcc tgctggttat ctacgtgtca tggaagcggt accctgcgag 1850

catgaagcag ctgcagcagc gctccctcat gcgaaggcac aggaaaaaga 1900

aaagacagtc cctaaagcaa atgactccca gcacccagga attttatgta 1950

gattataaac ccaccaacac ggagaccagc gagatgctgc tgaatgggac 2000

gggaccctgc acctataaca aatcgggctc caggggagtgt gaggtatgaa 2050

ccattgtgat aaaaagagct cttaaaagct gggaaataag tggtgcttta 2100
```

363

```
ttgaactctg gtgactatca agggaacgcg atgccccccc tcccctttccc 2150

tctccctctc actttggtgg caagatcctt ccttgtccgt tttagtgcat 2200

tcataatact ggtcattttc ctctcataca taatcaaccc attgaaattt 2250

aaataccaca atcaatgtga agcttgaact ccggtttaat ataataccta 2300

ttgtataaga ccctttactg attccattaa tgtcgcattt gttttaagat 2350

aaaacttctt tcataggtaa aaaaaaaaa 2379
```

<210> 385
<211> 513
<212> PRT
<213> Homo sapiens

<400> 385

```
Met Gly Phe Asn Val Ile Arg Leu Leu Ser Gly Ser Ala Val Ala
  1               5                  10                  15

Leu Val Ile Ala Pro Thr Val Leu Leu Thr Met Leu Ser Ser Ala
             20                  25                  30

Glu Arg Gly Cys Pro Lys Gly Cys Arg Cys Glu Gly Lys Met Val
             35                  40                  45

Tyr Cys Glu Ser Gln Lys Leu Gln Glu Ile Pro Ser Ser Ile Ser
             50                  55                  60

Ala Gly Cys Leu Gly Leu Ser Leu Arg Tyr Asn Ser Leu Gln Lys
             65                  70                  75

Leu Lys Tyr Asn Gln Phe Lys Gly Leu Asn Gln Leu Thr Trp Leu
             80                  85                  90

Tyr Leu Asp His Asn His Ile Ser Asn Ile Asp Glu Asn Ala Phe
             95                  100                 105

Asn Gly Ile Arg Arg Leu Lys Glu Leu Ile Leu Ser Ser Asn Arg
             110                 115                 120

Ile Ser Tyr Phe Leu Asn Asn Thr Phe Arg Pro Val Thr Asn Leu
             125                 130                 135

Arg Asn Leu Asp Leu Ser Tyr Asn Gln Leu His Ser Leu Gly Ser
             140                 145                 150

Glu Gln Phe Arg Gly Leu Arg Lys Leu Leu Ser Leu His Leu Arg
             155                 160                 165

Ser Asn Ser Leu Arg Thr Ile Pro Val Arg Ile Phe Gln Asp Cys
             170                 175                 180

Arg Asn Leu Glu Leu Leu Asp Leu Gly Tyr Asn Arg Ile Arg Ser
             185                 190                 195

Leu Ala Arg Asn Val Phe Ala Gly Met Ile Arg Leu Lys Glu Leu
```

His Leu Glu His Asn Gln Phe Ser Lys Leu Asn Leu Ala Leu Phe
           215   220   225

Pro Arg Leu Val Ser Leu Gln Asn Leu Tyr Leu Gln Trp Asn Lys
           230   235   240

Ile Ser Val Ile Gly Gln Thr Met Ser Trp Thr Trp Ser Ser Leu
           245   250   255

Gln Arg Leu Asp Leu Ser Gly Asn Glu Ile Glu Ala Phe Ser Gly
           260   265   270

Pro Ser Val Phe Gln Cys Val Pro Asn Leu Gln Arg Leu Asn Leu
           275   280   285

Asp Ser Asn Lys Leu Thr Phe Ile Gly Gln Glu Ile Leu Asp Ser
           290   295   300

Trp Ile Ser Leu Asn Asp Ile Ser Leu Ala Gly Asn Ile Trp Glu
           305   310   315

Cys Ser Arg Asn Ile Cys Ser Leu Val Asn Trp Leu Lys Ser Phe
           320   325   330

Lys Gly Leu Arg Glu Asn Thr Ile Ile Cys Ala Ser Pro Lys Glu
           335   340   345

Leu Gln Gly Val Asn Val Ile Asp Ala Val Lys Asn Tyr Ser Ile
           350   355   360

Cys Gly Lys Ser Thr Thr Glu Arg Phe Asp Leu Ala Arg Ala Leu
           365   370   375

Pro Lys Pro Thr Phe Lys Pro Lys Leu Pro Arg Pro Lys His Glu
           380   385   390

Ser Lys Pro Pro Leu Pro Pro Thr Val Gly Ala Thr Glu Pro Gly
           395   400   405

Pro Glu Thr Asp Ala Asp Ala Glu His Ile Ser Phe His Lys Ile
           410   415   420

Ile Ala Gly Ser Val Ala Leu Phe Leu Ser Val Leu Val Ile Leu
           425   430   435

Leu Val Ile Tyr Val Ser Trp Lys Arg Tyr Pro Ala Ser Met Lys
           440   445   450

Gln Leu Gln Gln Arg Ser Leu Met Arg Arg His Arg Lys Lys Lys
           455   460   465

Arg Gln Ser Leu Lys Gln Met Thr Pro Ser Thr Gln Glu Phe Tyr
           470   475   480

Val Asp Tyr Lys Pro Thr Asn Thr Glu Thr Ser Glu Met Leu Leu
           485   490   495

```
Asn Gly Thr Gly Pro Cys Thr Tyr Asn Lys Ser Gly Ser Arg Glu
          500                     505                     510

Cys Glu Val


<210> 386
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 386
 ctgggatctg aacagtttcg gggc 24

<210> 387
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 387
 ggtccccagg acatggtctg tccc 24

<210> 388
<211> 48
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-48
<223> Synthetic construct.

<400> 388
 gctgagttta catttacggt ctaactccct gagaaccatc cctgtgcg 48

<210> 389
<211> 1449
<212> DNA
<213> Homo sapiens

<400> 389
 agttctgaga aagaaggaaa taaacacagg caccaaacca ctatcctaag 50

 ttgactgtcc tttaaatatg tcaagatcca gacttttcag tgtcacctca 100

 gcgatctcaa cgatagggat cttgtgtttg ccgctattcc agttggtgct 150

 ctcggaccta ccatgcgaag aagatgaaat gtgtgtaaat tataatgacc 200
```

```
aacaccctaa tggctggtat atctggatcc tcctgctgct ggttttggtg 250

gcagctcttc tctgtggagc tgtggtcctc tgcctccagt gctggctgag 300

gagaccccga attgattctc acaggcgcac catggcagtt tttgctgttg 350

gagacttgga ctctatttat gggacagaag cagctgtgag tccaactgtt 400

ggaattcacc ttcaaactca aacccctgac ctatatcctg ttcctgctcc 450

atgttttggc cctttaggct ccccacctcc atatgaagaa attgtaaaaa 500

caacctgatt ttaggtgtgg attatcaatt taaagtatta acgacatctg 550

taattccaaa acatcaaatt taggaatagt tatttcagtt gttggaaatg 600

tccagagatc tattcatata gtctgaggaa ggacaattcg acaaaagaat 650

ggatgttgga aaaattttg gtcatggaga tgtttaaata gtaaagtagc 700

aggcttttga tgtgtcactg ctgtatcata cttttatgct acacaaccaa 750

attaatgctt ctccactagt atccaaacag gcaacaatta ggtgctggaa 800

gtagtttcca tcacatttag gactccactg cagtatacag cacaccattt 850

tctgctttaa actctttcct agcatggggt ccataaaaat tattataatt 900

taacaatagc ccaagccgag aatccaacat gtccagaacc agaaccagaa 950

agatagtatt tgaatgaagg tgaggggaga gagtaggaaa aagaaaagtt 1000

tggagttgaa gggtaaagga taaatgaaga ggaaaaggaa aagattacaa 1050

gtctcagcaa aaacaagagg ttttatgccc caacctgaag aggaagaaat 1100

tgtagataga aggtgaagga gattgctgaa gatatagagc acatataatg 1150

ccaacacggg gagaaaagaa aatttcccct tttacagtaa tgaatgtggc 1200

ctccatagtc catagtgttt ctctggagcc tcagggcttg gcatttattg 1250

cagcatcatg ctaagaacct tcggcatagg tatctgttcc catgaggact 1300

gcagaagtag caatgagaca tcttcaagtg gcattttggc agtggccatc 1350

agcaggggga cagacaaaaa catccatcac agatgacata tgatcttcag 1400

ctgacaaatt tgttgaacaa aacaataaac atcaatagat atctaaaaa 1449

<210> 390
<211> 146
<212> PRT
<213> Homo sapiens

<400> 390
Met Ser Arg Ser Arg Leu Phe Ser Val Thr Ser Ala Ile Ser Thr
1               5                   10                  15
```

```
Ile Gly Ile Leu Cys Leu Pro Leu Phe Gln Leu Val Leu Ser Asp
              20                  25                      30

Leu Pro Cys Glu Glu Asp Glu Met Cys Val Asn Tyr Asn Asp Gln
              35                  40                      45

His Pro Asn Gly Trp Tyr Ile Trp Ile Leu Leu Leu Val Leu
              50                  55                      60

Val Ala Ala Leu Leu Cys Gly Ala Val Val Leu Cys Leu Gln Cys
              65                  70                      75

Trp Leu Arg Arg Pro Arg Ile Asp Ser His Arg Arg Thr Met Ala
              80                  85                      90

Val Phe Ala Val Gly Asp Leu Asp Ser Ile Tyr Gly Thr Glu Ala
              95                  100                     105

Ala Val Ser Pro Thr Val Gly Ile His Leu Gln Thr Gln Thr Pro
              110                 115                     120

Asp Leu Tyr Pro Val Pro Ala Pro Cys Phe Gly Pro Leu Gly Ser
              125                 130                     135

Pro Pro Pro Tyr Glu Glu Ile Val Lys Thr Thr
              140                 145
```

<210> 391
<211> 26
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-26
<223> Synthetic construct.

<400> 391
 cttttcagtg tcacctcagc gatctc 26

<210> 392
<211> 23
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-23
<223> Synthetic construct.

<400> 392
 ccaaaacatg gagcaggaac agg 23

<210> 393
<211> 47
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-47
<223> Synthetic construct.

<400> 393
ccagttggtg ctctcggacc taccatgcga agaagatgaa atgtgtg 47

<210> 394
<211> 2340
<212> DNA
<213> Homo sapiens

<400> 394
gagcggagta aaatctccac aagctgggaa caaacctcgt cccaactccc 50

acccaccggc gtttctccag ctcgatctgg aggctgcttc gccagtgtgg 100

gacgcagctg acgcccgctt attagctctc gctgcgtcgc cccggctcag 150

aagctccgtg gcggcggcga ccgtgacgag aagcccacgg ccagctcagt 200

tctcttctac tttgggagag agagaaagtc agatgcccct tttaaactcc 250

ctcttcaaaa ctcatctcct gggtgactga gttaatagag tggatacaac 300

cttgctgaag atgaagaata tacaatattg aggatatttt tttctttttt 350

ttttcaagtc ttgatttgtg gcttacctca agttaccatt tttcagtcaa 400

gtctgtttgt ttgcttcttc agaaatgttt tttacaatct caagaaaaaa 450

tatgtcccag aaattgagtt tactgttgct tgtatttgga ctcatttggg 500

gattgatgtt actgcactat acttttcaac aaccaagaca tcaaagcagt 550

gtcaagttac gtgagcaaat actagactta agcaaaagat atgttaaagc 600

tctagcagag gaaaataaga acacagtgga tgtcgagaac ggtgcttcta 650

tggcaggata tgcggatctg aaaagaacaa ttgctgtcct tctggatgac 700

attttgcaac gattggtgaa gctggagaac aaagttgact atattgttgt 750

gaatggctca gcagccaaca ccaccaatgg tactagtggg aatttggtgc 800

cagtaaccac aaataaaaga acgaatgtct cgggcagtat cagatagcag 850

ttgaaaatca ccttgtgctg ctccatccac tgtggattat atcctatggc 900

agaaaagctt tataattgct ggcttaggac agagcaatac tttacaataa 950

aagctctaca cattttcaag gagtatgctg gattcatgga actctaattc 1000

tgtacataaa aattttaaag ttatttgttt gctttcaggc aagtctgttc 1050

aatgctgtac tatgtcctta aagagaattt ggtaacttgg ttgatgtggt 1100

369

```
aagcagatag gtgagttttg tataaatctt ttgtgtttga gatcaagctg 1150

aaatgaaaac actgaaaaac atggattcat ttctataaca catttatttа 1200

agtatataac acgttttttg dacaagtgaa gaatgtttaa tcattctgtc 1250

atttgttctc aatagatgta actgttagac tacggctatt tgaaaaaatg 1300

tgcttattgt actatatttt gttattccaa ttatgagcag agaaaggaaa 1350

tataatgttg aaaataatgt tttgaaatca tgacccaaag aatgtattga 1400

tttgcactat ccttcagaat aactgaaggt taattattgt atatttttaa 1450

aaattacact tataagagta taatcttgaa atgggtagca gccactgtcc 1500

attacctatc gtaaacattg gggcaattta ataacagcat taaaatagtt 1550

gtaaactcta atcttatact tattgaagaa taaaagatat ttttatgatg 1600

agagtaacaa taaagtattc atgattttc acatacatga atgttcattt 1650

aaaagtttaa tcctttgagt gtctatgcta tcaggaaagc acattatttc 1700

catatttggg ttaattttgc ttttattata ttggtctagg aggaagggac 1750

tttggagaat ggaactcttg aggactttag ccaggtgtat ataataaagg 1800

tacttttgtg ctgcattaaa ttgcttggaa agtgttaaca ttatattata 1850

taagagtatc ctttatgaaa ttttgaattt gtataacaga tgcattagat 1900

attcatttta tataatggcc acttaaaata agaacattta aaatataaac 1950

tatgaagatt gactatcttt tcaggaaaaa agctgtatat agcacaggga 2000

accctaatct tgggtaattc tagtataaaa caaattatac ttttatttaa 2050

atttcccttg tagcaaatct aattgccaca tggtgcccta tatttcatag 2100

tatttattct ctatagtaac tgcttaagtg cagctagctt ctagatttag 2150

actatataga atttagatat tgtattgttc gtcattataa tatgctacca 2200

catgtagcaa taattacaat attttattaa aataaatatg tgaaatattg 2250

tttcatgaaa gacagatttc caaatctctc ttctcttctc tgtactgtct 2300

acctttatgt gaagaaatta attatatgcc attgccaggt 2340
```

<210> 395
<211> 140
<212> PRT
<213> Homo sapiens

<400> 395
Met Phe Phe Thr Ile Ser Arg Lys Asn Met Ser Gln Lys Leu Ser
 1   5   10   15

```
Leu Leu Leu Leu Val Phe Gly Leu Ile Trp Gly Leu Met Leu Leu
            20                  25                  30

His Tyr Thr Phe Gln Gln Pro Arg His Gln Ser Ser Val Lys Leu
            35                  40                  45

Arg Glu Gln Ile Leu Asp Leu Ser Lys Arg Tyr Val Lys Ala Leu
            50                  55                  60

Ala Glu Glu Asn Lys Asn Thr Val Asp Val Glu Asn Gly Ala Ser
            65                  70                  75

Met Ala Gly Tyr Ala Asp Leu Lys Arg Thr Ile Ala Val Leu Leu
            80                  85                  90

Asp Asp Ile Leu Gln Arg Leu Val Lys Leu Glu Asn Lys Val Asp
            95                  100                 105

Tyr Ile Val Val Asn Gly Ser Ala Ala Asn Thr Thr Asn Gly Thr
            110                 115                 120

Ser Gly Asn Leu Val Pro Val Thr Thr Asn Lys Arg Thr Asn Val
            125                 130                 135

Ser Gly Ser Ile Arg
            140
```

<210> 396
<211> 2639
<212> DNA
<213> Homo sapiens

<400> 396
```
cgcggccggg ccgccggggt gagcgtgccg aggcggctgt ggcgcaggct 50

tccagccccc accatgccgt ggcccctgct gctgctgctg gccgtgagtg 100

gggcccagac aacccggcca tgcttccccg ggtgccaatg cgaggtggag 150

accttcggcc ttttcgacag cttcagcctg actcgggtgg attgtagcgg 200

cctgggcccc cacatcatgc cggtgcccat ccctctggac acagcccact 250

tggacctgtc ctccaaccgg ctggagatgg tgaatgagtc ggtgttggcg 300

gggccgggct acacgacgtt ggctggcctg atctcagcc acaacctgct 350

caccagcatc tcacccactg ccttctcccg ccttcgctac ctggagtcgc 400

ttgacctcag ccacaatggc ctgacagccc tgccagccga gagcttcacc 450

agctcacccc tgagcgacgt gaaccttagc cacaaccagc tccgggaggt 500

ctcagtgtct gccttcacga cgcacagtca gggccgggca ctacacgtgg 550

acctctccca caacctcatt caccgcctcg tgccccaccc cacgagggcc 600

ggcctgcctg cgcccaccat tcagagcctg aacctggcct ggaaccggct 650
```

371

```
ccatgccgtg cccaacctcc gagacttgcc cctgcgctac ctgagcctgg 700

atgggaaccc tctagctgtc attggtccgg gtgccttcgc ggggctggga 750

ggccttacac acctgtctct ggccagcctg cagaggctcc ctgagctggc 800

gcccagtggc ttccgtgagc taccgggcct gcaggtcctg gacctgtcgg 850

gcaaccccaa gcttaactgg gcaggagctg aggtgttttc aggcctgagc 900

tccctgcagg agctggacct ttcgggcacc aacctggtgc ccctgcctga 950

ggcgctgctc ctccacctcc cggcactgca gagcgtcagc gtgggccagg 1000

atgtgcggtg ccggcgcctg gtgcgggagg gcacctaccc ccggaggcct 1050

ggctccagcc ccaaggtgcc cctgcactgc gtagacaccc gggaatctgc 1100

tgccaggggc cccaccatct tgtgacaaat ggtgtggccc agggccacat 1150

aacagactgc tgtcctgggc tgcctcaggt cccgagtaac ttatgttcaa 1200

tgtgccaaca ccagtgggga gcccgcaggc ctatgtggca gcgtcaccac 1250

aggagttgtg ggcctaggag aggctttgga cctgggagcc acacctagga 1300

gcaaagtctc acccctttgt ctacgttgct tccccaaacc atgagcagag 1350

ggacttcgat gccaaaccag actcgggtcc cctcctgctt cccttcccca 1400

cttatccccc aagtgccttc cctcatgcct gggccggcct gacccgcaat 1450

gggcagaggg tgggtgggac cccctgctgc agggcagagt tcaggtccac 1500

tgggctgagt gtccccttgg gcccatggcc cagtcactca ggggcgagtt 1550

tcttttctaa catagccctt tctttgccat gaggccatga ggcccgcttc 1600

atccttttct atttccctag aaccttaatg gtagaaggaa ttgcaaagaa 1650

tcaagtccac ccttctcatg tgacagatgg ggaaactgag gccttgagaa 1700

ggaaaaaggc taatctaagt tcctgcgggc agtggcatga ctggagcaca 1750

gcctcctgcc tcccagcccg gacccaatgc actttcttgt ctcctctaat 1800

aagccccacc ctccccgcct gggctcccct tgctgccctt gcctgttccc 1850

cattagcaca ggagtagcag cagcaggaca ggcaagagcc tcacaagtgg 1900

gactctgggc ctctgaccag ctgtgcggca tgggctaagt cactctgccc 1950

ttcggagcct ctggaagctt agggcacatt ggttccagcc tagccagttt 2000

ctcaccctgg gttggggtcc cccagcatcc agactggaaa cctacccatt 2050

ttcccctgag catcctctag atgctgcccc aaggagttgc tgcagttctg 2100
```

372

```
gagcctcatc tggctgggat ctccaagggg cctcctggat tcagtcccca 2150

ctggccctga gcacgacagc ccttcttacc ctcccaggaa tgccgtgaaa 2200

ggagacaagg tctgcccgac ccatgtctat gctctacccc cagggcagca 2250

tctcagcttc cgaaccctgg gctgtttcct tagtcttcat tttataaaag 2300

ttgttgcctt tttaacggag tgtcactttc aaccggcctc ccctacccct 2350

gctggccggg gatggagaca tgtcatttgt aaaagcagaa aaaggttgca 2400

tttgttcact tttgtaatat tgtcctgggc ctgtgttggg gtgttggggg 2450

aagctgggca tcagtggcca catgggcatc aggggctggc cccacagaga 2500

ccccacaggg cagtgagctc tgtcttcccc cacctgccta gcccatcatc 2550

tatctaaccg gtccttgatt taataaacac tataaaggt ttaaaaaaa 2600

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaa 2639
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<210> 397
<211> 353
<212> PRT
<213> Homo sapiens

<400> 397

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Met Pro Trp Pro Leu Leu Leu Leu Ala Val Ser Gly Ala Gln
  1           5                  10                  15

Thr Thr Arg Pro Cys Phe Pro Gly Cys Gln Cys Glu Val Glu Thr
                20              25                  30

Phe Gly Leu Phe Asp Ser Phe Ser Leu Thr Arg Val Asp Cys Ser
                35              40                  45

Gly Leu Gly Pro His Ile Met Pro Val Pro Ile Pro Leu Asp Thr
                50              55                  60

Ala His Leu Asp Leu Ser Ser Asn Arg Leu Glu Met Val Asn Glu
                65              70                  75

Ser Val Leu Ala Gly Pro Gly Tyr Thr Thr Leu Ala Gly Leu Asp
                80              85                  90

Leu Ser His Asn Leu Leu Thr Ser Ile Ser Pro Thr Ala Phe Ser
                95              100                 105

Arg Leu Arg Tyr Leu Glu Ser Leu Asp Leu Ser His Asn Gly Leu
                110             115                 120

Thr Ala Leu Pro Ala Glu Ser Phe Thr Ser Ser Pro Leu Ser Asp
                125             130                 135

Val Asn Leu Ser His Asn Gln Leu Arg Glu Val Ser Val Ser Ala
                140             145                 150
```

373

```
Phe Thr Thr His Ser Gln Gly Arg Ala Leu His Val Asp Leu Ser
            155                 160                 165

His Asn Leu Ile His Arg Leu Val Pro His Pro Thr Arg Ala Gly
            170                 175                 180

Leu Pro Ala Pro Thr Ile Gln Ser Leu Asn Leu Ala Trp Asn Arg
            185                 190                 195

Leu His Ala Val Pro Asn Leu Arg Asp Leu Pro Leu Arg Tyr Leu
            200                 205                 210

Ser Leu Asp Gly Asn Pro Leu Ala Val Ile Gly Pro Gly Ala Phe
            215                 220                 225

Ala Gly Leu Gly Gly Leu Thr His Leu Ser Leu Ala Ser Leu Gln
            230                 235                 240

Arg Leu Pro Glu Leu Ala Pro Ser Gly Phe Arg Glu Leu Pro Gly
            245                 250                 255

Leu Gln Val Leu Asp Leu Ser Gly Asn Pro Lys Leu Asn Trp Ala
            260                 265                 270

Gly Ala Glu Val Phe Ser Gly Leu Ser Ser Leu Gln Glu Leu Asp
            275                 280                 285

Leu Ser Gly Thr Asn Leu Val Pro Leu Pro Glu Ala Leu Leu Leu
            290                 295                 300

His Leu Pro Ala Leu Gln Ser Val Ser Val Gly Gln Asp Val Arg
            305                 310                 315

Cys Arg Arg Leu Val Arg Glu Gly Thr Tyr Pro Arg Arg Pro Gly
            320                 325                 330

Ser Ser Pro Lys Val Pro Leu His Cys Val Asp Thr Arg Glu Ser
            335                 340                 345

Ala Ala Arg Gly Pro Thr Ile Leu
            350
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<210> 398
<211> 23
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-23
<223> Synthetic construct.

<400> 398
 ccctgccagc cgagagcttc acc 23

<210> 399
<211> 23
<212> DNA

<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-23
<223> Synthetic construct.

<400> 399
 ggttggtgcc cgaaaggtcc agc 23

<210> 400
<211> 44
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-44
<223> Synthetic construct.

<400> 400
 caaccccaag cttaactggg caggagctga ggtgttttca ggcc 44

<210> 401
<211> 1571
<212> DNA
<213> Homo sapiens

<400> 401
 gatggcgcag ccacagcttc tgtgagattc gatttctccc cagttcccct 50

 gtgggtctga ggggaccaga agggtgagct acgttggctt tctggaaggg 100

 gaggctatat gcgtcaattc cccaaaacaa gttttgacat ttcccctgaa 150

 atgtcattct ctatctattc actgcaagtg cctgctgttc caggccttac 200

 ctgctgggca ctaacggcgg agccaggatg gggacagaat aaaggagcca 250

 cgacctgtgc caccaactcg cactcagact ctgaactcag acctgaaatc 300

 ttctcttcac gggaggcttg gcagtttttc ttactcctgt ggtctccaga 350

 tttcaggcct aagatgaaag cctctagtct tgccttcagc cttctctctg 400

 ctgcgtttta tctcctatgg actccttcca ctggactgaa gacactcaat 450

 ttgggaagct gtgtgatcgc cacaaacctt caggaaatac gaaatggatt 500

 ttctgagata cggggcagtg tgcaagccaa agatggaaac attgacatca 550

 gaatcttaag gaggactgag tctttgcaag acacaaagcc tgcgaatcga 600

 tgctgcctcc tgcgccattt gctaagactc tatctggaca gggtatttaa 650

 aaactaccag accccctgacc attatactct ccggaagatc agcagcctcg 700

 ccaattcctt tcttaccatc aagaaggacc tccggctctc tcatgcccac 750

375

```
atgacatgcc attgtgggga ggaagcaatg aagaaataca gccagattct 800

gagtcacttt gaaaagctgg aacctcaggc agcagttgtg aaggctttgg 850

gggaactaga cattcttctg caatggatgg aggagacaga ataggaggaa 900

agtgatgctg ctgctaagaa tattcgaggt caagagctcc agtcttcaat 950

acctgcagag gaggcatgac cccaaaccac catctcttta ctgtactagt 1000

cttgtgctgg tcacagtgta tcttatttat gcattacttg cttccttgca 1050

tgattgtctt tatgcatccc caatcttaat tgagaccata cttgtataag 1100

attttttgtaa tatctttctg ctattggata tatttattag ttaatatatt 1150

tatttatttt ttgctatttta atgtatttat ttttttactt ggacatgaaa 1200

ctttaaaaaa attcacagat tatatttata acctgactag agcaggtgat 1250

gtatttttat acagtaaaaa aaaaaaacct tgtaaattct agaagagtgg 1300

ctagggggggt tattcatttg tattcaacta aggacatatt tactcatgct 1350

gatgctctgt gagatatttg aaattgaacc aatgactact taggatgggt 1400

tgtggaataa gttttgatgt ggaattgcac atctacctta caattactga 1450

ccatccccag tagactcccc agtcccataa ttgtgtatct tccagccagg 1500

aatcctacac ggccagcatg tatttctaca aataaagttt tctttgcata 1550

ccaaaaaaaa aaaaaaaaaa a 1571

<210> 402
<211> 261
<212> PRT
<213> Homo sapiens

<400> 402
  Met Arg Gln Phe Pro Lys Thr Ser Phe Asp Ile Ser Pro Glu Met
  1               5                   10                  15

  Ser Phe Ser Ile Tyr Ser Leu Gln Val Pro Ala Val Pro Gly Leu
                  20                  25                  30

  Thr Cys Trp Ala Leu Thr Ala Glu Pro Gly Trp Gly Gln Asn Lys
                  35                  40                  45

  Gly Ala Thr Thr Cys Ala Thr Asn Ser His Ser Asp Ser Glu Leu
                  50                  55                  60

  Arg Pro Glu Ile Phe Ser Ser Arg Glu Ala Trp Gln Phe Phe Leu
                  65                  70                  75

  Leu Leu Trp Ser Pro Asp Phe Arg Pro Lys Met Lys Ala Ser Ser
                  80                  85                  90
```

376

```
Leu Ala Phe Ser Leu Leu Ser Ala Ala Phe Tyr Leu Leu Trp Thr
                    95                  100                 105

Pro Ser Thr Gly Leu Lys Thr Leu Asn Leu Gly Ser Cys Val Ile
                110                 115                 120

Ala Thr Asn Leu Gln Glu Ile Arg Asn Gly Phe Ser Glu Ile Arg
                125                 130                 135

Gly Ser Val Gln Ala Lys Asp Gly Asn Ile Asp Ile Arg Ile Leu
                140                 145                 150

Arg Arg Thr Glu Ser Leu Gln Asp Thr Lys Pro Ala Asn Arg Cys
                155                 160                 165

Cys Leu Leu Arg His Leu Leu Arg Leu Tyr Leu Asp Arg Val Phe
                170                 175                 180

Lys Asn Tyr Gln Thr Pro Asp His Tyr Thr Leu Arg Lys Ile Ser
                185                 190                 195

Ser Leu Ala Asn Ser Phe Leu Thr Ile Lys Lys Asp Leu Arg Leu
                200                 205                 210

Ser His Ala His Met Thr Cys His Cys Gly Glu Glu Ala Met Lys
                215                 220                 225

Lys Tyr Ser Gln Ile Leu Ser His Phe Glu Lys Leu Glu Pro Gln
                230                 235                 240

Ala Ala Val Val Lys Ala Leu Gly Glu Leu Asp Ile Leu Leu Gln
                245                 250                 255

Trp Met Glu Glu Thr Glu
                260

<210> 403
<211> 28
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-28
<223> Synthetic construct.

<400> 403
 ctcctgtggt ctccagattt caggccta 28

<210> 404
<211> 26
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-26
<223> Synthetic construct.
```

<400> 404
 agtcctcctt aagattctga tgtcaa 26

<210> 405
<211> 998
<212> DNA
<213> Homo sapiens

<400> 405
 ccgttatcgt cttgcgctac tgctgaatgt ccgtcccgga ggaggaggag 50

 aggcttttgc cgctgaccca gagatggccc cgagcgagca aattcctact 100

 gtccggctgc gcggctaccg tggccgagct agcaaccttt cccctggatc 150

 tcacaaaaac tcgactccaa atgcaaggag aagcagctct tgctcggttg 200

 ggagacggtg caagagaatc tgccccctat aggggaatgg tgcgcacagc 250

 cctagggatc attgaagagg aaggctttct aaagctttgg caaggagtga 300

 cacccgccat ttacagacac gtagtgtatt ctggaggtcg aatggtcaca 350

 tatgaacatc tccgagaggt tgtgtttggc aaaagtgaag atgagcatta 400

 tcccctttgg aaatcagtca ttggagggat gatggctggt gttattggcc 450

 agttttttagc caatccaact gacctagtga aggttcagat gcaaatggaa 500

 ggaaaaagga aactggaagg aaaaccattg cgatttcgtg gtgtacatca 550

 tgcatttgca aaaatcttag ctgaₑggagg aatacgaggg ctttgggcag 600

 gctgggtacc caatatacaa agagcagcac tggtgaatat gggagattta 650

 accacttatg atacagtgaa acactacttg gtattgaata caccacttga 700

 ggacaatatc atgactcacg gtttatcaag tttatgttct ggactggtag 750

 cttctattct gggaacacca gccgatgtca tcaaaagcag aataatgaat 800

 caaccacgag ataaacaagg aaggggactt ttgtataaat catcgactga 850

 ctgcttgatt caggctgttc aaggtgaagg attcatgagt ctatataaag 900

 gcttttttacc atcttggctg agaatgaccc cttggtcaat ggtgttctgg 950

 cttacttatg aaaaaatcag agagatgagt ggagtcagtc cattttaa 998

<210> 406
<211> 323
<212> PRT
<213> Homo sapiens

<400> 406
 Met Ser Val Pro Glu Glu Glu Arg Leu Leu Pro Leu Thr Gln
  1   5   10   15

378

Arg Trp Pro Arg Ala Ser Lys Phe Leu Leu Ser Gly Cys Ala Ala
              20   25   30

Thr Val Ala Glu Leu Ala Thr Phe Pro Leu Asp Leu Thr Lys Thr
              35   40   45

Arg Leu Gln Met Gln Gly Glu Ala Ala Leu Ala Arg Leu Gly Asp
              50   55   60

Gly Ala Arg Glu Ser Ala Pro Tyr Arg Gly Met Val Arg Thr Ala
              65   70   75

Leu Gly Ile Ile Glu Glu Glu Gly Phe Leu Lys Leu Trp Gln Gly
              80   85   90

Val Thr Pro Ala Ile Tyr Arg His Val Val Tyr Ser Gly Gly Arg
              95   100   105

Met Val Thr Tyr Glu His Leu Arg Glu Val Val Phe Gly Lys Ser
             110   115   120

Glu Asp Glu His Tyr Pro Leu Trp Lys Ser Val Ile Gly Gly Met
             125   130   135

Met Ala Gly Val Ile Gly Gln Phe Leu Ala Asn Pro Thr Asp Leu
             140   145   150

Val Lys Val Gln Met Gln Met Glu Gly Lys Arg Lys Leu Glu Gly
             155   160   165

Lys Pro Leu Arg Phe Arg Gly Val His His Ala Phe Ala Lys Ile
             170   175   180

Leu Ala Glu Gly Gly Ile Arg Gly Leu Trp Ala Gly Trp Val Pro
             185   190   195

Asn Ile Gln Arg Ala Ala Leu Val Asn Met Gly Asp Leu Thr Thr
             200   205   210

Tyr Asp Thr Val Lys His Tyr Leu Val Leu Asn Thr Pro Leu Glu
             215   220   225

Asp Asn Ile Met Thr His Gly Leu Ser Ser Leu Cys Ser Gly Leu
             230   235   240

Val Ala Ser Ile Leu Gly Thr Pro Ala Asp Val Ile Lys Ser Arg
             245   250   255

Ile Met Asn Gln Pro Arg Asp Lys Gln Gly Arg Gly Leu Leu Tyr
             260   265   270

Lys Ser Ser Thr Asp Cys Leu Ile Gln Ala Val Gln Gly Glu Gly
             275   280   285

Phe Met Ser Leu Tyr Lys Gly Phe Leu Pro Ser Trp Leu Arg Met
             290   295   300

Thr Pro Trp Ser Met Val Phe Trp Leu Thr Tyr Glu Lys Ile Arg

379

Glu Met Ser Gly Val Ser Pro Phe
                      320

<210> 407
<211> 31
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-31
<223> Synthetic construct.

<400> 407
 cgcggatccc gttatcgtct tgcgctactg c 31

<210> 408
<211> 34
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-34
<223> Synthetic construct.

<400> 408
 gcggaattct taaaatggac tgactccact catc 34

<210> 409
<211> 1487
<212> DNA
<213> Homo sapiens

<400> 409
 cggacgcgtg ggcgcgggac gccggcaggg ttgtggcgca gcagtctcct 50

 tcctgcgcgc gcgcctgaag tcggcgtggg cgtttgagga agctgggata 100

 cagcatttaa tgaaaaattt atgcttaaga agtaaaaatg gcaggcttcc 150

 tagataattt tcgttggcca gaatgtgaat gtattgactg gagtgagaga 200

 agaaatgctg tggcatctgt tgtcgcaggt atattgtttt ttacaggctg 250

 gtggataatg attgatgcag ctgtggtgta tcctaagcca gaacagttga 300

 accatgcctt tcacacatgt ggtgtatttt ccacattggc tttcttcatg 350

 ataaatgctg tatccaatgc tcaggtgaga ggtgatagct atgaaagcgg 400

 ctgtttagga agaacaggtg ctcgagtttg cttttcatt ggtttcatgt 450

 tgatgtttgg gtcacttatt gcttccatgt ggattctttt tggtgcatat 500

 gttacccaaa atactgatgt ttatccggga ctagctgtgt tttttcaaaa 550

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tgcacttata ttttttagca ctctgatcta caaatttgga agaaccgaag 600

agctatggac ctgagatcac ttcttaagtc acattttcct tttgttatat 650

tctgtttgta gataggtttt ttatctctca gtacacattg ccaaatggag 700

tagattgtac attaaatgtt ttgtttcttt acatttttat gttctgagtt 750

ttgaaatagt tttatgaaat ttctttattt ttcattgcat agactgttaa 800

tatgtatata atacaagact atatgaattg gataatgagt atcagttttt 850

tattcctgag atttagaact tgatctactc cctgagccag ggttacatca 900

tcttgtcatt ttagaagtaa ccactcttgt ctctctggct gggcacggtg 950

gctcatgcct gtaatcccag cactttggga ggccgaggcg ggccgattgc 1000

ttgaggtcaa gtgtttgaga ccagcctggc caacatggcg aaaccccatc 1050

tactaaaaat acaaaaatta gccaggcatg gtggtgggtg cctgtaatcc 1100

cagctacctg ggaggctgag gcaggagaat cgcttgaacc cggggggcag 1150

aggttgcagt gagctgagtt tgcgccactg cactctagcc tggggagaa 1200

agtgaaactc cctctcaaaa aaaagaccac tctcagtatc tctgatttct 1250

gaagatgtac aaaaaaatat agcttcatat atctggaatg agcactgagc 1300

cataaaaggt tttcagcaag ttgtaactta ttttggccta aaaatgaggt 1350

ttttttggta aagaaaaaat atttgttctt atgtattgaa gaagtgtact 1400

tttatataat gattttttaa atgcccaaag gactagtttg aaagcttctt 1450

ttaaaaagaa ttcctctaat atgactttat gtgagaa 1487
```

<210> 410
<211> 158
<212> PRT
<213> Homo sapiens

<400> 410
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Met Ala Gly Phe Leu Asp Asn Phe Arg Trp Pro Glu Cys Glu Cys
1               5                   10                  15

Ile Asp Trp Ser Glu Arg Arg Asn Ala Val Ala Ser Val Val Ala
                20                  25                  30

Gly Ile Leu Phe Phe Thr Gly Trp Trp Ile Met Ile Asp Ala Ala
                35                  40                  45

Val Val Tyr Pro Lys Pro Glu Gln Leu Asn His Ala Phe His Thr
                50                  55                  60

Cys Gly Val Phe Ser Thr Leu Ala Phe Phe Met Ile Asn Ala Val
                65                  70                  75
```

Ser Asn Ala Gln Val Arg Gly Asp Ser Tyr Glu Ser Gly Cys Leu
              80   85   90

Gly Arg Thr Gly Ala Arg Val Trp Leu Phe Ile Gly Phe Met Leu
              95   100   105

Met Phe Gly Ser Leu Ile Ala Ser Met Trp Ile Leu Phe Gly Ala
             110   115   120

Tyr Val Thr Gln Asn Thr Asp Val Tyr Pro Gly Leu Ala Val Phe
             125   130   135

Phe Gln Asn Ala Leu Ile Phe Phe Ser Thr Leu Ile Tyr Lys Phe
             140   145   150

Gly Arg Thr Glu Glu Leu Trp Thr
             155

<210> 411
<211> 20
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-20
<223> Synthetic construct.

<400> 411
 gtttgaggaa gctgggatac 20

<210> 412
<211> 20
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-20
<223> Synthetic construct.

<400> 412
 ccaaactcga gcacctgttc 20

<210> 413
<211> 40
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-40
<223> Synthetic construct.

<400> 413
 atggcaggct tcctagataa ttttcgttgg ccagaatgtg 40

<210> 414

<211> 1337
<212> DNA
<213> Homo sapiens

<400> 414
gttgatggca aacttcctca aaggaggggc agagcctgcg cagggcagga 50

gcagctggcc cactggcggc ccgcaacact ccgtctcacc ctctgggccc 100

actgcatcta gaggagggcc gtctgtgagg ccactacccc tccagcaact 150

gggaggtggg actgtcagaa gctggcccag ggtggtggtc agctgggtca 200

gggacctacg gcacctgctg gaccacctcg ccttctccat cgaagcaggg 250

aagtgggagc ctcgagccct cgggtggaag ctgaccccaa gccacccttc 300

acctggacag gatgagagtg tcaggtgtgc ttcgcctcct ggccctcatc 350

tttgccatag tcacgacatg gatgtttatt cgaagctaca tgagcttcag 400

catgaaaacc atccgtctgc cacgctggct ggcagcctcg cccaccaagg 450

agatccaggt taaaaagtac aagtgtggcc tcatcaagcc ctgcccagcc 500

aactactttg cgtttaaaat ctgcagtggg gccgccaacg tcgtgggccc 550

tactatgtgc tttgaagacc gcatgatcat gagtcctgtg aaaaacaatg 600

tgggcagagg cctaaacatc gccctggtga atggaaccac gggagctgtg 650

ctgggacaga aggcatttga catgtactct ggagatgtta tgcacctagt 700

gaaattcctt aaagaaattc cgggggggtgc actggtgctg gtggcctcct 750

acgacgatcc agggaccaaa atgaacgatg aaagcaggaa actcttctct 800

gacttgggga gttcctacgc aaaacaactg ggcttccggg acagctgggt 850

cttcatagga gccaaagacc tcagggggtaa aagccccttt gagcagttct 900

taaagaacag cccagacaca aacaaatacg agggatggcc agagctgctg 950

gagatggagg gctgcatgcc cccgaagcca ttttagggtg gctgtggctc 1000

ttcctcagcc aggggcctga agaagctcct gcctgactta ggagtcagag 1050

cccggcaggg gctgaggagg aggagcaggg ggtgctgcgt ggaaggtgct 1100

gcaggtcctt gcacgctgtg tcgcgcctct cctcctcgga aacagaaccc 1150

tcccacagca catcctaccc ggaagaccag cctcagaggg tccttctgga 1200

accagctgtc tgtggagaga atggggtgct ttcgtcaggg actgctgacg 1250

gctggtcctg aggaaggaca aactgcccag acttgagccc aattaaattt 1300

tattttttgct ggttttgaaa aaaaaaaaa aaaaaaa 1337

<210> 415
<211> 224
<212> PRT
<213> Homo sapiens

<400> 415

```
Met Arg Val Ser Gly Val Leu Arg Leu Leu Ala Leu Ile Phe Ala
 1               5                  10                  15

Ile Val Thr Thr Trp Met Phe Ile Arg Ser Tyr Met Ser Phe Ser
                20                  25                  30

Met Lys Thr Ile Arg Leu Pro Arg Trp Leu Ala Ala Ser Pro Thr
                35                  40                  45

Lys Glu Ile Gln Val Lys Lys Tyr Lys Cys Gly Leu Ile Lys Pro
                50                  55                  60

Cys Pro Ala Asn Tyr Phe Ala Phe Lys Ile Cys Ser Gly Ala Ala
                65                  70                  75

Asn Val Val Gly Pro Thr Met Cys Phe Glu Asp Arg Met Ile Met
                80                  85                  90

Ser Pro Val Lys Asn Asn Val Gly Arg Gly Leu Asn Ile Ala Leu
                95                  100                 105

Val Asn Gly Thr Thr Gly Ala Val Leu Gly Gln Lys Ala Phe Asp
                110                 115                 120

Met Tyr Ser Gly Asp Val Met His Leu Val Lys Phe Leu Lys Glu
                125                 130                 135

Ile Pro Gly Gly Ala Leu Val Leu Val Ala Ser Tyr Asp Asp Pro
                140                 145                 150

Gly Thr Lys Met Asn Asp Glu Ser Arg Lys Leu Phe Ser Asp Leu
                155                 160                 165

Gly Ser Ser Tyr Ala Lys Gln Leu Gly Phe Arg Asp Ser Trp Val
                170                 175                 180

Phe Ile Gly Ala Lys Asp Leu Arg Gly Lys Ser Pro Phe Glu Gln
                185                 190                 195

Phe Leu Lys Asn Ser Pro Asp Thr Asn Lys Tyr Glu Gly Trp Pro
                200                 205                 210

Glu Leu Leu Glu Met Glu Gly Cys Met Pro Pro Lys Pro Phe
                215                 220
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<210> 416
<211> 21
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence

<222> 1-21
<223> Synthetic construct.

<400> 416
 gccatagtca cgacatggat g 21

<210> 417
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 417
 ggatggccag agctgctg 18

<210> 418
<211> 26
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-26
<223> Synthetic construct.

<400> 418
 aaagtacaag tgtggcctca tcaagc 26

<210> 419
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 419
 tctgactcct aagtcaggca ggag 24

<210> 420
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 420
 attctctcca cagacagctg gttc 24

<210> 421
<211> 46
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-46
<223> Synthetic construct.

<400> 421
gtacaagtgt ggcctcatca agccctgccc agccaactac tttgcg 46

<210> 422
<211> 1701
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 1528
<223> unknown base

<400> 422
gagactgcag agggagataa agagagaggg caaagaggca gcaagagatt 50

tgtcctgggg atccagaaac ccatgatacc ctactgaaca ccgaatcccc 100

tggaagccca cagagacaga gacagcaaga gaagcagaga taaatacact 150

cacgccagga gctcgctcgc tctctctctc tctctctcac tcctccctcc 200

ctctctctct gcctgtccta gtcctctagt cctcaaattc ccagtcccct 250

gcacccttc ctgggacact atgttgttct ccgccctcct gctggaggtg 300

atttggatcc tggctgcaga tgggggtcaa cactggacgt atgagggccc 350

acatggtcag gaccattggc cagcctctta ccctgagtgt ggaaacaatg 400

cccagtcgcc catcgatatt cagacagaca gtgtgacatt tgaccctgat 450

ttgcctgctc tgcagcccca cggatatgac cagcctggca ccgagccttt 500

ggacctgcac aacaatggcc acacagtgca actctctctg ccctctaccc 550

tgtatctggg tggacttccc cgaaaatatg tagctgccca gctccacctg 600

cactggggtc agaaaggatc cccagggggg tcagaacacc agatcaacag 650

tgaagccaca tttgcagagc tccacattgt acattatgac tctgattcct 700

atgacagctt gagtgaggct gctgagaggc ctcagggcct ggctgtcctg 750

ggcatcctaa ttgaggtggg tgagactaag aatatagctt atgaacacat 800

tctgagtcac ttgcatgaag tcaggcataa agatcagaag acctcagtgc 850

386

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ctcccttcaa cctaagagag ctgctcccca aacagctggg gcagtacttc 900

cgctacaatg gctcgctcac aactcccct tgctaccaga gtgtgctctg 950

gacagttttt tatagaaggt cccagatttc aatggaacag ctggaaaagc 1000

ttcaggggac attgttctcc acagaagagg agccctctaa gcttctggta 1050

cagaactacc gagcccttca gcctctcaat cagcgcatgg tctttgcttc 1100

tttcatccaa gcaggatcct cgtataccac aggtgaaatg ctgagtctag 1150

gtgtaggaat cttggttggc tgtctctgcc ttctcctggc tgtttatttc 1200

attgctagaa agattcggaa gaagaggctg gaaaaccgaa agagtgtggt 1250

cttcacctca gcacaagcca cgactgaggc ataaattcct tctcagatac 1300

catggatgtg gatgacttcc cttcatgcct atcaggaagc ctctaaaatg 1350

gggtgtagga tctggccaga aacactgtag gagtagtaag cagatgtcct 1400

ccttcccctg gacatctctt agagaggaat ggacccaggc tgtcattcca 1450

ggaagaactg cagagccttc agcctctcca aacatgtagg aggaaatgag 1500

gaaatcgctg tgttgttaat gcagaganca aactctgttt agttgcaggg 1550

gaagtttggg atatacccca aagtcctcta ccccctcact tttatggccc 1600

tttccctaga tatactgcgg gatctctcct taggataaag agttgctgtt 1650

gaagttgtat attttgatc aatatatttg gaaattaaag tttctgactt 1700

t 1701

<210> 423
<211> 337
<212> PRT
<213> Homo sapiens

<400> 423
Met Leu Phe Ser Ala Leu Leu Leu Glu Val Ile Trp Ile Leu Ala
 1               5                  10                  15

Ala Asp Gly Gly Gln His Trp Thr Tyr Glu Gly Pro His Gly Gln
                20                  25                  30

Asp His Trp Pro Ala Ser Tyr Pro Glu Cys Gly Asn Asn Ala Gln
                35                  40                  45

Ser Pro Ile Asp Ile Gln Thr Asp Ser Val Thr Phe Asp Pro Asp
                50                  55                  60

Leu Pro Ala Leu Gln Pro His Gly Tyr Asp Gln Pro Gly Thr Glu
                65                  70                  75

Pro Leu Asp Leu His Asn Asn Gly His Thr Val Gln Leu Ser Leu
```

387

Pro Ser Thr Leu Tyr Leu Gly Gly Leu Pro Arg Lys Tyr Val Ala
                    95   100   105

Ala Gln Leu His Leu His Trp Gly Gln Lys Gly Ser Pro Gly Gly
                   110   115   120

Ser Glu His Gln Ile Asn Ser Glu Ala Thr Phe Ala Glu Leu His
                   125   130   135

Ile Val His Tyr Asp Ser Asp Ser Tyr Asp Ser Leu Ser Glu Ala
                   140   145   150

Ala Glu Arg Pro Gln Gly Leu Ala Val Leu Gly Ile Leu Ile Glu
                   155   160   165

Val Gly Glu Thr Lys Asn Ile Ala Tyr Glu His Ile Leu Ser His
                   170   175   180

Leu His Glu Val Arg His Lys Asp Gln Lys Thr Ser Val Pro Pro
                   185   190   195

Phe Asn Leu Arg Glu Leu Leu Pro Lys Gln Leu Gly Gln Tyr Phe
                   200   205   210

Arg Tyr Asn Gly Ser Leu Thr Thr Pro Pro Cys Tyr Gln Ser Val
                   215   220   225

Leu Trp Thr Val Phe Tyr Arg Arg Ser Gln Ile Ser Met Glu Gln
                   230   235   240

Leu Glu Lys Leu Gln Gly Thr Leu Phe Ser Thr Glu Glu Glu Pro
                   245   250   255

Ser Lys Leu Leu Val Gln Asn Tyr Arg Ala Leu Gln Pro Leu Asn
                   260   265   270

Gln Arg Met Val Phe Ala Ser Phe Ile Gln Ala Gly Ser Ser Tyr
                   275   280   285

Thr Thr Gly Glu Met Leu Ser Leu Gly Val Gly Ile Leu Val Gly
                   290   295   300

Cys Leu Cys Leu Leu Leu Ala Val Tyr Phe Ile Ala Arg Lys Ile
                   305   310   315

Arg Lys Lys Arg Leu Glu Asn Arg Lys Ser Val Val Phe Thr Ser
                   320   325   330

Ala Gln Ala Thr Thr Glu Ala
                   335

<210> 424
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 424
gtaaagtcgc tggccagc 18

<210> 425
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 425
cccgatctgc ctgctgta 18

<210> 426
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 426
ctgcactgta tggccattat tgtg 24

<210> 427
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 427
cagaaaccca tgatacccta ctgaacaccg aatcccctgg aagcc 45

<210> 428
<211> 1073
<212> DNA
<213> Homo sapiens

<400> 428
aattttttcac cagagtaaac ttgagaaacc aactggacct tgagtattgt 50

acattttgcc tcgtggaccc aaaggtagca atctgaaaca tgaggagtac 100

gattctactg ttttgtcttc taggatcaac tcggtcatta ccacagctca 150

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aacctgcttt gggactccct cccacaaaac tggctccgga tcagggaaca 200

ctaccaaacc aacagcagtc aaatcaggtc tttccttctt taagtctgat 250

accattaaca cagatgctca cactgggggcc agatctgcat ctgttaaatc 300

ctgctgcagg aatgacacct ggtacccaga cccacccatt gaccctggga 350

gggttgaatg tacaacagca actgcaccca catgtgttac caatttttgt 400

cacacaactt ggagcccagg gcactatcct aagctcagag gaattgccac 450

aaatcttcac gagcctcatc atccattcct tgttcccggg aggcatcctg 500

cccaccagtc aggcaggggc taatccagat gtccaggatg gaagccttcc 550

agcaggagga gcaggtgtaa atcctgccac ccagggaacc ccagcaggcc 600

gcctcccaac tcccagtggc acagatgacg actttgcagt gaccacccct 650

gcaggcatcc aaaggagcac acatgccatc gaggaagcca ccacagaatc 700

agcaaatgga attcagtaag ctgtttcaaa ttttttcaac taagctgcct 750

cgaatttggt gatacatgtg aatctttatc attgattata ttatggaata 800

gattgagaca cattggatag tcttagaaga aattaattct taatttacct 850

gaaaatattc ttgaaatttc agaaaatatg ttctatgtag agaatcccaa 900

cttttaaaaa caataattca atggataaat ctgtctttga aatataacat 950

tatgctgcct ggatgatatg catattaaaa catatttgga aaactggaaa 1000

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1050

aaaaaaaaaa aaaaaaaaaa aaa 1073
```

<210> 429
<211> 209
<212> PRT
<213> Homo sapiens

<400> 429

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Met Arg Ser Thr Ile Leu Leu Phe Cys Leu Leu Gly Ser Thr Arg
 1               5                  10                  15

Ser Leu Pro Gln Leu Lys Pro Ala Leu Gly Leu Pro Pro Thr Lys
            20                  25                  30

Leu Ala Pro Asp Gln Gly Thr Leu Pro Asn Gln Gln Ser Asn
                35              40                  45

Gln Val Phe Pro Ser Leu Ser Leu Ile Pro Leu Thr Gln Met Leu
                50              55                  60

Thr Leu Gly Pro Asp Leu His Leu Leu Asn Pro Ala Ala Gly Met
                65              70                  75
```

390

```
Thr Pro Gly Thr Gln Thr His Pro Leu Thr Leu Gly Gly Leu Asn
            80                  85                      90

Val Gln Gln Gln Leu His Pro His Val Leu Pro Ile Phe Val Thr
            95              100                     105

Gln Leu Gly Ala Gln Gly Thr Ile Leu Ser Ser Glu Glu Leu Pro
            110             115                     120

Gln Ile Phe Thr Ser Leu Ile Ile His Ser Leu Phe Pro Gly Gly
            125             130                     135

Ile Leu Pro Thr Ser Gln Ala Gly Ala Asn Pro Asp Val Gln Asp
            140             145                     150

Gly Ser Leu Pro Ala Gly Gly Ala Gly Val Asn Pro Ala Thr Gln
            155             160                     165

Gly Thr Pro Ala Gly Arg Leu Pro Thr Pro Ser Gly Thr Asp Asp
            170             175                     180

Asp Phe Ala Val Thr Thr Pro Ala Gly Ile Gln Arg Ser Thr His
            185             190                     195

Ala Ile Glu Glu Ala Thr Thr Glu Ser Ala Asn Gly Ile Gln
            200             205
```

<210> 430
<211> 1257
<212> DNA
<213> Homo Sapien

<400> 430
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ggagagaggc gcgcgggtga aaggcgcatt gatgcagcct gcggcggcct 50
cggagcgcgg cggagccaga cgctgaccac gttcctctcc tcggtctcct 100
ccgcctccag ctccgcgctg cccggcagcc gggagccatg cgaccccagg 150
gccccgccgc ctccccgcag cggctccgcg gcctcctgct gctcctgctg 200
ctgcagctgc ccgcgccgtc gagcgcctct gagatcccca aggggaagca 250
aaaggcgcag ctccggcaga gggaggtggt ggacctgtat aatggaatgt 300
gcttacaagg gccagcagga gtgcctggtc gagacgggag ccctgggggcc 350
aatgttattc cgggtacacc tgggatccca ggtcgggatg gattcaaagg 400
agaaaagggg gaatgtctga gggaaagctt tgaggagtcc tggacaccca 450
actacaagca gtgttcatgg agttcattga attatggcat agatcttggg 500
aaaattgcgg agtgtacatt tacaaagatg cgttcaaata gtgctctaag 550
agttttgttc agtggctcac ttcggctaaa atgcagaaat gcatgctgtc 600
agcgttggta tttcacattc aatggagctg aatgttcagg acctcttccc 650
```

391

attgaagcta taatttattt ggaccaagga agccctgaaa tgaattcaac 700

aattaatatt catcgcactt cttctgtgga aggactttgt gaaggaattg 750

gtgctggatt agtggatgtt gctatctggg ttggcacttg ttcagattac 800

ccaaaaggag atgcttctac tggatggaat tcagtttctc gcatcattat 850

tgaagaacta ccaaaataaa tgctttaatt ttcatttgct acctcttttt 900

ttattatgcc ttggaatggt tcacttaaat gacattttaa ataagtttat 950

gtatacatct gaatgaaaag caaagctaaa tatgtttaca gaccaaagtg 1000

tgatttcaca ctgttttttaa atctagcatt attcattttg cttcaatcaa 1050

aagtggtttc aatatttttt ttagttggtt agaatacttt cttcatagtc 1100

acattctctc aacctataat ttggaatatt gttgtggtct tttgtttttt 1150

ctcttagtat agcattttta aaaaaatata aaagctacca atctttgtac 1200

aatttgtaaa tgttaagaat ttttttttata tctgttaaat aaaaattatt 1250

tccaaca 1257

<210> 431
<211> 243
<212> PRT
<213> Homo Sapien

<400> 431
Met Arg Pro Gln Gly Pro Ala Ala Ser Pro Gln Arg Leu Arg Gly
1   5   10   15

Leu Leu Leu Leu Leu Leu Leu Gln Leu Pro Ala Pro Ser Ser Ala
                20   25   30

Ser Glu Ile Pro Lys Gly Lys Gln Lys Ala Gln Leu Arg Gln Arg
                35   40   45

Glu Val Val Asp Leu Tyr Asn Gly Met Cys Leu Gln Gly Pro Ala
                50   55   60

Gly Val Pro Gly Arg Asp Gly Ser Pro Gly Ala Asn Val Ile Pro
                65   70   75

Gly Thr Pro Gly Ile Pro Gly Arg Asp Gly Phe Lys Gly Glu Lys
                80   85   90

Gly Glu Cys Leu Arg Glu Ser Phe Glu Glu Ser Trp Thr Pro Asn
                95   100   105

Tyr Lys Gln Cys Ser Trp Ser Ser Leu Asn Tyr Gly Ile Asp Leu
                110   115   120

Gly Lys Ile Ala Glu Cys Thr Phe Thr Lys Met Arg Ser Asn Ser
                125   130   135

392

```
Ala Leu Arg Val Leu Phe Ser Gly Ser Leu Arg Leu Lys Cys Arg
              140                 145                 150

Asn Ala Cys Cys Gln Arg Trp Tyr Phe Thr Phe Asn Gly Ala Glu
              155                 160                 165

Cys Ser Gly Pro Leu Pro Ile Glu Ala Ile Ile Tyr Leu Asp Gln
              170                 175                 180

Gly Ser Pro Glu Met Asn Ser Thr Ile Asn Ile His Arg Thr Ser
              185                 190                 195

Ser Val Glu Gly Leu Cys Glu Gly Ile Gly Ala Gly Leu Val Asp
              200                 205                 210

Val Ala Ile Trp Val Gly Thr Cys Ser Asp Tyr Pro Lys Gly Asp
              215                 220                 225

Ala Ser Thr Gly Trp Asn Ser Val Ser Arg Ile Ile Ile Glu Glu
              230                 235                 240

Leu Pro Lys


<210> 432
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificial Sequence

<400> 432
 aggacttgcc ctcaggaa 18

<210> 433
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 433
 cgcaggacag ttgtgaaaat a 21

<210> 434
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 434
 atgacgctcg tccaaggcca c 21

<210> 435
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<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 435
 cccacctgta ccaccatgt 19

<210> 436
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 436
 actccaggca ccatctgttc tccc 24

<210> 437
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 437
 aagggctggc attcaagtc 19

<210> 438
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 438
 tgacctggca aaggaagaa 19

<210> 439
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 439
 cagccaccct ccagtccaag g 21

<210> 440
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 440
gggtcgtgtt ttggagaga 19

<210> 441
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 441
ctggccctca gagcaccaat 20

<210> 442
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 442
tcctccatca cttcccctag ctcca 25

<210> 443
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 443
ctggcaggag ttaaagttcc aaga 24

<210> 444
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 444
aaaggacacc gggatgtg 18

<210> 445
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 445
agcgtacact ctctccaggc aaccag 26

<210> 446
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 446
caattctgga tgaggtggta ga 22

<210> 447
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 447
caggactgag cgcttgttta 20

<210> 448
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 448
caaagcgcca agtaccggac c 21

<210> 449
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 449
ccagacctca gccaggaa 18

<210> 450
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 450
ccctagctga ccccttca 18

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<210> 451
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 451
 tctgacaagc agttttctga atc 23

<210> 452
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 452
 ctctccccct cccttttcct ttgttt 26

<210> 453
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 453
 ctctggtgcc cacagtga 18

<210> 454
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 454
 ccatgcctgc tcagccaaga a 21

<210> 455
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 455
 caggaaatct ggaaacctac agt 23

<210> 456
<211> 20
<212> DNA
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<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 456
ccttgaaaag gacccagttt 20

<210> 457
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 457
atgagtcgca cctgctgttc cc 22

<210> 458
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 458
tagcagctgc ccttggta 18

<210> 459
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 459
aacagcaggt gcgactcatc ta 22

<210> 460
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 460
tgctaggcga cgacacccag acc 23

<210> 461
<211> 18
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 461
tggacacgtg gcagtgga 18

<210> 462
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 462
tcatggtctc gtcccattc 19

<210> 463
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 463
caccatttgt ttctctgtct ccccatc 27

<210> 464
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 464
ccggcatcct tggagtag 18

<210> 465
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 465
tccccattag cacaggagta 20

<210> 466
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 466

aggctcttgc ctgtcctgct gct 23

<210> 467
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 467
 gcccagagtc ccacttgt 18

<210> 468
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 468
 actgctccgc ctactacga 19

<210> 469
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 469
 aggcatcctc gccgtcctca 20

<210> 470
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 470
 aaggccaagg tgagtccat 19

<210> 471
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 471
 cgagtgtgtg cgaaacctaa 20

<210> 472

<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 472
 tcagggtcta catcagcctc ctgc 24

<210> 473
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 473
 aaggccaagg tgagtccat 19

<210> 474
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 474
 cctactgagg agccctatgc 20

<210> 475
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 475
 tccaggtgga ccccacttca gg 22

<210> 476
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 476
 gggaggctta taggcccaat ctgg 24

<210> 477
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 477
 ggcttcagca gcacgtgtga agtcgaagtc gcagtcacag atatcaatga 50